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(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as ovarian cancer, are disclosed. Compositions may comprise one or more ovarian carcinoma proteins, immunogenic portions thereof, polynucleotides that encode such portions or antibodies or immune system cells specific for such proteins. Such compositions may be used, for example, for the prevention and treatment of diseases such as ovarian cancer. Methods are further provided for identifying tumor antigens that are secreted from ovarian carcinomas and/or other tumors. Polypeptides and polynucleotides as provided herein may further be used for the diagnosis and monitoring of ovarian cancer.

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(74) Agents: **POTTER, Jane, E., R.**; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 et al. (US).

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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

Technical Field

The present invention relates generally to ovarian cancer therapy. The invention is more specifically related to polypeptides comprising at least a portion of an ovarian carcinoma protein, and to polynucleotides encoding such polypeptides, as well as antibodies and immune system cells that specifically recognize such polypeptides. Such polypeptides, polynucleotides, antibodies and cells may be used in vaccines and pharmaceutical compositions for treatment of ovarian cancer.

10 Background of the Invention

Ovarian cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and therapy of this cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Management of the disease currently relies on a combination of early diagnosis and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. However, the use of established markers often leads to a result that is difficult to interpret, and high mortality continues to be observed in many cancer patients.

Immunotherapies have the potential to substantially improve cancer treatment and survival. Such therapies may involve the generation or enhancement of an immune response to an ovarian carcinoma antigen. However, to date, relatively few ovarian carcinoma antigens are known and the generation of an immune response against such antigens has not been shown to be therapeutically beneficial.

Accordingly, there is a need in the art for improved methods for identifying ovarian tumor antigens and for using such antigens in the therapy of ovarian cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, this invention provides compositions and methods for the therapy of cancer, such as ovarian cancer. In one aspect, the present invention provides polypeptides comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished. Within certain embodiments, the ovarian carcinoma protein comprises a sequence that is encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NO:456-457, 460-477 and 512-570 and complements of such polynucleotides.

The present invention further provides polynucleotides that encode a polypeptide as described above or a portion thereof, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

The present invention further provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596.

Within other aspects, the present invention provides pharmaceutical compositions and vaccines. Pharmaceutical compositions may comprise a physiologically acceptable carrier or excipient in combination with one or more of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence encoded by a polynucleotide that comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570 or (ii) a polynucleotide encoding such a polypeptide; (iii) an antibody that specifically binds to such a polypeptide; (iv) an antigen-presenting cell that expresses such a polypeptide and/or (v) a T cell that specifically reacts with such a polypeptide. Vaccines may comprise a non-specific immune response enhancer in combination with one or more of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions

and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence set forth in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596 or an amino acid sequence encoded by a polynucleotide that
5 comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570 or (ii) a polynucleotide encoding such a polypeptide; (iii) an anti-idiotypic antibody that is specifically bound by an antibody that specifically binds to such a polypeptide; (iv) an antigen-presenting cell that expresses such a polypeptide and/or (v) a T cell that specifically reacts with such a polypeptide.

10 The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

 Within related aspects, pharmaceutical compositions comprising a fusion protein or polynucleotide encoding a fusion protein in combination with a
15 physiologically acceptable carrier are provided.

 Vaccines are further provided, within other aspects, comprising a fusion protein or polynucleotide encoding a fusion protein in combination with a non-specific immune response enhancer.

 Within further aspects, the present invention provides methods for
20 inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

 The present invention further provides, within other aspects, methods for stimulating and/or expanding T cells, comprising contacting T cells with (a) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a
25 variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence set forth in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596 or an amino acid sequence encoded by a polynucleotide that comprises a
30 sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570; (b) a polynucleotide encoding such a polypeptide and/or (c) an antigen presenting cell that

expresses such a polypeptide under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Such polypeptide, polynucleotide and/or antigen presenting cell(s) may be present within a pharmaceutical composition or vaccine, for use in stimulating and/or expanding T cells in a mammal.

5 Within other aspects, the present invention provides methods for inhibiting the development of ovarian cancer in a patient, comprising administering to a patient T cells prepared as described above.

 Within further aspects, the present invention provides methods for inhibiting the development of ovarian cancer in a patient, comprising the steps of: (a)
10 incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein
15 comprises an amino acid sequence encoded by a polynucleotide that comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570; (ii) a polynucleotide encoding such a polypeptide; or (iii) an antigen-presenting cell that expresses such a polypeptide; such that T cells proliferate; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the
20 development of ovarian cancer in the patient. The proliferated cells may be cloned prior to administration to the patient.

 The present invention also provides, within other aspects, methods for identifying secreted tumor antigens. Such methods comprise the steps of: (a) implanting tumor cells in an immunodeficient mammal; (b) obtaining serum from the
25 immunodeficient mammal after a time sufficient to permit secretion of tumor antigens into the serum; (c) immunizing an immunocompetent mammal with the serum; (d) obtaining antiserum from the immunocompetent mammal; and (e) screening a tumor expression library with the antiserum, and therefrom identifying a secreted tumor antigen. A preferred method for identifying a secreted ovarian carcinoma antigen
30 comprises the steps of: (a) implanting ovarian carcinoma cells in a SCID mouse; (b) obtaining serum from the SCID mouse after a time sufficient to permit secretion of

ovarian carcinoma antigens into the serum; (c) immunizing an immunocompetent mouse with the serum; (d) obtaining antiserum from the immunocompetent mouse; and (e) screening an ovarian carcinoma expression library with the antiserum, and therefrom identifying a secreted ovarian carcinoma antigen.

5 The present invention also discloses antibody epitopes recognized by the O8E polyclonal anti-sera which epitopes are presented herein as SEQ ID NO: 394-415.

Further disclosed by the present invention are 10-mer and 9-mer peptides predicted to bind HLA-0201 which peptides are disclosed herein as SEQ ID NO:416-435 and SEQ ID NO:436-455, respectively.

10 These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

In another aspect of the present invention, the applicants have
15 unexpectedly identified a series of novel repeating sequence elements in the 5' end of the gene encoding O772P. Therefore, the present invention provides O772P polypeptides having structures represented by X_n -Y, wherein X comprises a sequence having at least 50% identity, preferably at least 70% identity, and more preferably at least 90% identity with an O772P repeat sequence set forth in SEQ ID NO: 596. Y will
20 typically comprise a sequence having at least 80% identity, preferably at least 90% identity and more preferably at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 594. According to this embodiment, n will generally be an integer from 1 to 35, preferably an integer from 15 to 25, and X can be the same or different.

25 In one preferred embodiment, X comprises a sequence selected from the group consisting of any one of SEQ ID NOs: 574-593 and Y comprises the sequence set forth in SEQ ID NO: 594.

In another preferred embodiment, an illustrative O772P polypeptide comprises the sequence set forth in SEQ ID NO: 595, containing 20 repeating sequence
30 elements (i.e., X_{20}) wherein the X elements are arranged in the following order (moving from N-terminal to C-terminal in the O772P repeat region): SEQ ID NO: 574 - SEQ ID

NO: 575 - SEQ ID NO: 576 - SEQ ID NO: 577 - SEQ ID NO: 578 - SEQ ID NO: 579 -
SEQ ID NO: 580 - SEQ ID NO: 581 - SEQ ID NO: 582 - SEQ ID NO: 583 - SEQ ID
NO: 584 - SEQ ID NO: 585 - SEQ ID NO: 586 - SEQ ID NO: 587 - SEQ ID NO: 588 -
SEQ ID NO: 589 - SEQ ID NO: 590 - SEQ ID NO: 591 - SEQ ID NO: 592 - SEQ ID
5 NO: 593.

According to another aspect of the present invention, an O772P polynucleotide is provided having the structure X_n -Y, wherein X comprises an O772P repeat sequence element selected from the group consisting of any one of SEQ ID NOs: 512-540, 542-546 and 548-567. Y will generally comprise a sequence having at least
10 80% identity, preferably at least 90% identity, and more preferably at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 568. In this embodiment, n is typically an integer from 1 to 35, preferably from 15 to 25 and X can be the same or different.

In another embodiment, an illustrative O772P polynucleotide comprises
15 the sequence set forth in SEQ ID NO: 569, containing 20 repeating sequence elements (i.e., X_{20}).

According to another aspect of the present invention, O772 polypeptides are provided comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 490-511.

20 According to another aspect of the present invention, O8E polypeptides are provided comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 394-415.

BRIEF DESCRIPTION OF THE SEQUENCE IDENTIFIERS AND DRAWINGS

SEQ ID NO:1-71 are ovarian carcinoma antigen polynucleotides shown
25 in Figures 1A-1S.

SEQ ID NO:72-74 are ovarian carcinoma antigen polynucleotides shown in Figures 2A-2C.

SEQ ID NO:75 is the ovarian carcinoma polynucleotide 3g (Figure 4).

SEQ ID NO:76 is the ovarian carcinoma polynucleotide 3f (Figure 5):

30 SEQ ID NO:77 is the ovarian carcinoma polynucleotide 6b (Figure 6).

SEQ ID NO:78 is the ovarian carcinoma polynucleotide 8e (Figure 7A).

SEQ ID NO:79 is the ovarian carcinoma polynucleotide 8h (Figure 7B).

SEQ ID NO:80 is the ovarian carcinoma polynucleotide 12e (Figure 8).

SEQ ID NO:81 is the ovarian carcinoma polynucleotide 12h (Figure 9).

5 SEQ ID NO:82-310 are ovarian carcinoma antigen polynucleotides shown in Figures 15A-15EEE.

SEQ ID NO:311 is a full length sequence of ovarian carcinoma polynucleotide O772P.

SEQ ID NO:312 is the O772P amino acid sequence.

10 SEQ ID NO:313-384 are ovarian carcinoma antigen polynucleotides.

SEQ ID NO:385 represents the cDNA sequence of a form of the clone O772P, designated 21013.

SEQ ID NO:386 represents the cDNA sequence of a form of the clone O772P, designated 21003.

15 SEQ ID NO:387 represents the cDNA sequence of a form of the clone O772P, designated 21008.

SEQ ID NOs:388 is the amino acid sequence corresponding to SEQ ID NO:385.

SEQ ID NOs:389 is the amino acid sequence corresponding to SEQ ID NO:386. SEQ ID NOs:390 is the amino acid sequence corresponding to SEQ ID NO:387.

SEQ ID NO:391 is a full length sequence of ovarian carcinoma polynucleotide O8E.

SEQ ID NO:392-393 are protein sequences encoded by O8E.

25 SEQ ID NO:394-415 are peptide sequences corresponding to the OE8 antibody epitopes.

SEQ ID NO:416-435 are potential HLA-A2 10-mer binding peptides predicted using the full length open-reading frame from OE8.

SEQ ID NO:436-455 are potential HLA-A2 9-mer binding peptides predicted using the full length open-reading frame from OE8.

30

SEQ ID NO:456 is a truncated nucleotide sequence of the full length Genbank sequence showing homology to O772P

SEQ ID NO:457 is the full length Genbank sequence showing significant homology to O772P

5 SEQ ID NO:458 is a protein encoding a truncated version of the full length Genbank sequence showing homology to O772P

SEQ ID NO:459 is the full length protein sequence from Genbank showing significant homology to the protein sequence for O772P

10 SEQ ID NO:460 encodes a unique N-terminal portion of O772P contained in residues 1-70.

SEQ ID NO:461 contains unique sequence and encodes residues 1-313 of SEQ ID NO: 456.

SEQ ID NO:462 is the hypothetical sequence for clone O772P.

SEQ ID NO:463 is the cDNA sequence for clone FLJ14303.

15 SEQ ID NO:464 is a partial cDNA sequence for clone O772P.

SEQ ID NO:465 is a partial cDNA sequence for clone O772P.

SEQ ID NO:466 is a partial cDNA sequence for clone O772P.

SEQ ID NO:467 is a partial cDNA sequence for clone O772P.

SEQ ID NO:468 is a partial cDNA sequence for clone O772P.

20 SEQ ID NO:469 is a partial cDNA sequence for clone O772P.

SEQ ID NO:470 is a partial cDNA sequence for clone O772P.

SEQ ID NO:471 is a partial cDNA sequence for clone O772P.

SEQ ID NO:472 is a partial cDNA sequence for clone O772P.

SEQ ID NO:473 is a partial cDNA sequence for clone O772P.

25 SEQ ID NO:474 is a partial cDNA sequence for clone O772P.

SEQ ID NO:475 is a partial cDNA sequence for clone O772P.

SEQ ID NO:476 is a partial cDNA sequence for clone O772P.

SEQ ID NO:477 represents the novel 5'-end of the ovarian tumor antigen O772P.

30 SEQ ID NO:478 is the amino acid sequence encoded by SEQ ID NO:462.

SEQ ID NO:479 is the amino acid sequence encoded by SEQ ID NO:463.

SEQ ID NO:480 is a partial amino acid sequence encoded by SEQ ID NO:472.

5 SEQ ID NO:481 is a partial amino acid sequence encoded by a possible open reading frame of SEQ ID NO:471.

SEQ ID NO:482 is a partial amino acid sequence encoded by a second possible open reading frame of SEQ ID NO:471.

10 SEQ ID NO:483 is a partial amino acid sequence encoded by SEQ ID NO:467.

SEQ ID NO:484 is a partial amino acid sequence encoded by a possible open reading frame of SEQ ID NO:466.

SEQ ID NO:485 is a partial amino acid sequence encoded by a second possible open reading frame of SEQ ID NO:466.

15 SEQ ID NO:486 is a partial amino acid sequence encoded by SEQ ID NO:465.

SEQ ID NO:487 is a partial amino acid sequence encoded by SEQ ID NO:464.

20 SEQ ID NO:488 represents the extracellular, transmembrane and cytoplasmic regions of O772P.

SEQ ID NO:489 represents the predicted extracellular domain of O772P.

SEQ ID NO:490 represents the amino acid sequence of peptide #2 which corresponds to an O772P specific antibody epitope.

25 SEQ ID NO:491 represents the amino acid sequence of peptide #6 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:492 represents the amino acid sequence of peptide #7 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:493 represents the amino acid sequence of peptide #8 which corresponds to an O772P specific antibody epitope.

30 SEQ ID NO:494 represents the amino acid sequence of peptide #9 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:495 represents the amino acid sequence of peptide #11 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:496 represents the amino acid sequence of peptide #13 which corresponds to an O772P specific antibody epitope.

5 SEQ ID NO:497 represents the amino acid sequence of peptide #22 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:498 represents the amino acid sequence of peptide #24 which corresponds to an O772P specific antibody epitope.

10 SEQ ID NO:499 represents the amino acid sequence of peptide #27 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:500 represents the amino acid sequence of peptide #40 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:501 represents the amino acid sequence of peptide #41 which corresponds to an O772P specific antibody epitope.

15 SEQ ID NO:502 represents the amino acid sequence of peptide #47 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:503 represents the amino acid sequence of peptide #50 which corresponds to an O772P specific antibody epitope.

20 SEQ ID NO:504 represents the amino acid sequence of peptide #51 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:505 represents the amino acid sequence of peptide #52 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:506 represents the amino acid sequence of peptide #53 which corresponds to an O772P specific antibody epitope.

25 SEQ ID NO:507 represents the amino acid sequence of peptide #58 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:508 represents the amino acid sequence of peptide #59 which corresponds to an O772P specific antibody epitope.

30 SEQ ID NO:509 represents the amino acid sequence of peptide #60 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:510 represents the amino acid sequence of peptide #61 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:511 represents the amino acid sequence of peptide #71 which corresponds to an O772P specific antibody epitope.

5 SEQ ID NO:512 (O772P repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:513 (O772P repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

10 SEQ ID NO:514 (O772P repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:515 (O772P repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:516 (O772P repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

15 SEQ ID NO:517 (HB repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:518 (HB repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

20 SEQ ID NO:519 (HB repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:520 (HB repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:521 (HB repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

25 SEQ ID NO:522 (HB repeat6 5'-end) represents an example of a cDNA sequence corresponding to repeat number 16 from the 5' variable region of O772P.

SEQ ID NO:523 (1043400.1 repeat1) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

30 SEQ ID NO:524 (1043400.1 repeat2) represents an example of a cDNA sequence corresponding to repeat number 10 from the 5' variable region of O772P.

SEQ ID NO:525 (1043400.1 repeat3) represents an example of a cDNA sequence corresponding to repeat number 10/11 from the 5' variable region of O772P.

SEQ ID NO:526 (1043400.1 repeat4) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

5 SEQ ID NO:527 (1043400.1 repeat5) represents an example of a cDNA sequence corresponding to repeat number 14 from the 5' variable region of O772P.

SEQ ID NO:528 (1043400.1 repeat6) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

10 SEQ ID NO:529 (1043400.3 repeat1) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

SEQ ID NO:530 (1043400.3 repeat2) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:531 (1043400.5 repeat1) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

15 SEQ ID NO:532 (1043400.5 repeat2) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P, in addition containing intron sequence.

SEQ ID NO:533 (1043400.5 repeat2) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

20 SEQ ID NO:534 (1043400.8 repeat1) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

SEQ ID NO:535 (1043400.8 repeat2) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

25 SEQ ID NO:536 (1043400.8 repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:537 (1043400.9 repeat1) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:538 (1043400.9 repeat2) represents an example of a cDNA sequence corresponding to repeat number 5 from the 5' variable region of O772P.

30 SEQ ID NO:539 (1043400.9 repeat3) represents an example of a cDNA sequence corresponding to repeat number 7 from the 5' variable region of O772P.

SEQ ID NO:540 (1043400.9 repeat4) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:541 (1043400.11 repeat1) represents an example of a cDNA sequence corresponding to repeat number 1 from the 5' variable region of O772P.

5 SEQ ID NO:542 (1043400.11 repeat2) represents an example of a cDNA sequence corresponding to repeat number 2 from the 5' variable region of O772P.

SEQ ID NO:543 (1043400.11 repeat3) represents an example of a cDNA sequence corresponding to repeat number 3 from the 5' variable region of O772P.

10 SEQ ID NO:544 (1043400.11 repeat4) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

SEQ ID NO:545 (1043400.11 repeat5) represents an example of a cDNA sequence corresponding to repeat number 12 from the 5' variable region of O772P.

SEQ ID NO:546 (1043400.12 repeat1) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

15 SEQ ID NO:547 (PB repeatA) represents an example of a cDNA sequence corresponding to repeat number 1 from the 5' variable region of O772P.

SEQ ID NO:548 (PB repeatB) represents an example of a cDNA sequence corresponding to repeat number 2 from the 5' variable region of O772P.

20 SEQ ID NO:549 (PB repeatE) represents an example of a cDNA sequence corresponding to repeat number 3 from the 5' variable region of O772P.

SEQ ID NO:550 (PB repeatG) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:551 (PB repeatC) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

25 SEQ ID NO:552 (PB repeatH) represents an example of a cDNA sequence corresponding to repeat number 6 from the 5' variable region of O772P.

SEQ ID NO:553 (PB repeatJ) represents an example of a cDNA sequence corresponding to repeat number 7 from the 5' variable region of O772P.

30 SEQ ID NO:554 (PB repeatK) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:555 (PB repeatD) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

SEQ ID NO:556 (PB repeatI) represents an example of a cDNA sequence corresponding to repeat number 10 from the 5' variable region of O772P.

5 SEQ ID NO:557 (PB repeatM) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

SEQ ID NO:558 (PB repeat9) represents an example of a cDNA sequence corresponding to repeat number 12 from the 5' variable region of O772P.

10 SEQ ID NO:559 (PB repeat8.5) represents an example of a cDNA sequence corresponding to repeat number 13 from the 5' variable region of O772P.

SEQ ID NO:560 (PB repeat8) represents an example of a cDNA sequence corresponding to repeat number 14 from the 5' variable region of O772P.

SEQ ID NO:561 (PB repeat7) represents an example of a cDNA sequence corresponding to repeat number 15 from the 5' variable region of O772P.

15 SEQ ID NO:562 (PB repeat6) represents an example of a cDNA sequence corresponding to repeat number 16 from the 5' variable region of O772P.

SEQ ID NO:563 (PB repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

20 SEQ ID NO:564 (PB repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:565 (PB repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:566 (PB repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

25 SEQ ID NO:567 (PB repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:568 represents the cDNA sequence form the 3' constant region.

30 SEQ ID NO:569 represents a cDNA sequence containing the consensus sequences of the 21 repeats, the 3' constant region and the 3' untranslated region.

SEQ ID NO:570 represents the cDNA sequence of the consensus repeat sequence.

SEQ ID NO:571 represents the consensus amino acid sequence of one potential open reading frame of repeat number 1 from the 5' variable region of O772P.

5 SEQ ID NO:572 represents the consensus amino acid sequence of a second potential open reading frame of repeat number 1 from the 5' variable region of O772P.

SEQ ID NO:573 represents the consensus amino acid sequence of a third potential open reading frame of repeat number 1 from the 5' variable region of O772P.

10 SEQ ID NO:574 represents the consensus amino acid sequence of repeat number 2 from the 5' variable region of O772P.

SEQ ID NO:575 represents the consensus amino acid sequence of repeat number 3 from the 5' variable region of O772P.

15 SEQ ID NO:576 represents the consensus amino acid sequence of repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:577 represents the consensus amino acid sequence of repeat number 5 from the 5' variable region of O772P.

SEQ ID NO:578 represents the consensus amino acid sequence of repeat number 6 from the 5' variable region of O772P.

20 SEQ ID NO:579 represents the consensus amino acid sequence of repeat number 7 from the 5' variable region of O772P.

SEQ ID NO:580 represents the consensus amino acid sequence of repeat number 8 from the 5' variable region of O772P.

25 SEQ ID NO:581 represents the consensus amino acid sequence of repeat number 9 from the 5' variable region of O772P.

SEQ ID NO:582 represents the consensus amino acid sequence of repeat number 10 from the 5' variable region of O772P.

SEQ ID NO:583 represents the consensus amino acid sequence of repeat number 11 from the 5' variable region of O772P.

30 SEQ ID NO:584 represents the consensus amino acid sequence of repeat number 12 from the 5' variable region of O772P.

SEQ ID NO:585 represents the consensus amino acid sequence of repeat number 13 from the 5' variable region of O772P.

SEQ ID NO:586 represents the consensus amino acid sequence of repeat number 14 from the 5' variable region of O772P.

5 SEQ ID NO:587 represents the consensus amino acid sequence of repeat number 15 from the 5' variable region of O772P.

SEQ ID NO:588 represents the consensus amino acid sequence of repeat number 16 from the 5' variable region of O772P.

10 SEQ ID NO:589 represents the consensus amino acid sequence of repeat number 17 from the 5' variable region of O772P.

SEQ ID NO:590 represents the consensus amino acid sequence of repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:591 represents the consensus amino acid sequence of repeat number 19 from the 5' variable region of O772P.

15 SEQ ID NO:592 represents the consensus amino acid sequence of repeat number 20 from the 5' variable region of O772P.

SEQ ID NO:593 represents the consensus amino acid sequence of repeat number 21 from the 5' variable region of O772P.

20 SEQ ID NO:594 represents the amino acid sequence of the 3' constant region.

SEQ ID NO:595 represents an amino acid sequence containing the consensus sequences of the 21 repeats and the 3' constant region.

SEQ ID NO:596 represents the amino acid sequence of the consensus repeat sequence.

25 Figures 1A-1S (SEQ ID NO:1-71) depict partial sequences of polynucleotides encoding representative secreted ovarian carcinoma antigens.

Figures 2A-2C depict full insert sequences for three of the clones of Figure 1. Figure 2A shows the sequence designated O7E (11731; SEQ ID NO:72), Figure 2B shows the sequence designated O9E (11785; SEQ ID NO:73) and Figure 2C
30 shows the sequence designated O8E (13695; SEQ ID NO:74).

Figure 3 presents results of microarray expression analysis of the ovarian carcinoma sequence designated O8E.

Figure 4 presents a partial sequence of a polynucleotide (designated 3g; SEQ ID NO:75) encoding an ovarian carcinoma sequence that is a splice fusion
5 between the human T-cell leukemia virus type I oncoprotein TAX and osteonectin.

Figure 5 presents the ovarian carcinoma polynucleotide designated 3f (SEQ ID NO:76).

Figure 6 presents the ovarian carcinoma polynucleotide designated 6b (SEQ ID NO:77).

10 Figures 7A and 7B present the ovarian carcinoma polynucleotides designated 8e (SEQ ID NO:78) and 8h (SEQ ID NO:79).

Figure 8 presents the ovarian carcinoma polynucleotide designated 12c (SEQ ID NO:80).

15 Figure 9 presents the ovarian carcinoma polynucleotide designated 12h (SEQ ID NO:81).

Figure 10 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 3f.

Figure 11 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 6b.

20 Figure 12 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 8e.

Figure 13 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 12c.

25 Figure 14 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 12h.

Figures 15A-15EEE depict partial sequences of additional polynucleotides encoding representative secreted ovarian carcinoma antigens (SEQ ID NO:82-310).

30 Figure 16 is a diagram illustrating the location of various partial O8E sequences within the full length sequence.

Figure 17 is a graph illustrating the results of epitope mapping studies on O8E protein.

Figure 18 is graph of a fluorescence activated cell sorting (FACS) analysis of O8E cell surface expression.

5 Figure 19 is graph of a FACS analysis of O8E cell surface expression.

Figure 20 shows FACS analysis results for O8E transfected HEK293 cells demonstrating cell surface expression of O8E.

Figure 21 shows FACS analysis results for SKBR3 breast tumor cells demonstrating cell surface expression of O8E.

10 Figure 22 shows O8E expression in HEK 293 cells. The cells were probed with anti-O8E rabbit polyclonal antisera #2333L.

Figure 23 shows the ELISA analysis of anti-O8E rabbit sera.

Figure 24 shows the ELISA analysis of affinity purified rabbit anti-O8E polyclonal antibody.

15 Figure 25 is a graph determining antibody internalization of anti-O8E mAb showing that mAbs against amino acids 61-80 induces ligand internalization.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy of cancer, such as ovarian cancer. The
20 compositions described herein may include immunogenic polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies that bind to a polypeptide, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells).

Polypeptides of the present invention generally comprise at least an immunogenic portion of an ovarian carcinoma protein or a variant thereof. Certain
25 ovarian carcinoma proteins have been identified using an immunoassay technique, and are referred to herein as ovarian carcinoma antigens. An "ovarian carcinoma antigen" is a protein that is expressed by ovarian tumor cells (preferably human cells) at a level that is at least two fold higher than the level in normal ovarian cells. Certain ovarian carcinoma antigens react detectably (within an immunoassay, such as an ELISA or
30 Western blot) with antisera generated against serum from an immunodeficient animal

implanted with a human ovarian tumor. Such ovarian carcinoma antigens are shed or secreted from an ovarian tumor into the sera of the immunodeficient animal. Accordingly, certain ovarian carcinoma antigens provided herein are secreted antigens. Certain nucleic acid sequences of the subject invention generally comprise a DNA or
5 RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence.

The present invention further provides ovarian carcinoma sequences that are identified using techniques to evaluate altered expression within an ovarian tumor. Such sequences may be polynucleotide or protein sequences. Ovarian carcinoma
10 sequences are generally expressed in an ovarian tumor at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal ovarian tissue, as determined using a representative assay provided herein. Certain partial ovarian carcinoma polynucleotide sequences are presented herein. Proteins encoded by genes comprising such polynucleotide sequences (or complements thereof) are also
15 considered ovarian carcinoma proteins.

Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to at least a portion of an ovarian carcinoma polypeptide as described herein. T cells that may be employed within the compositions provided herein are generally T cells (*e.g.*, CD4⁺ and/or CD8⁺) that are
20 specific for such a polypeptide. Certain methods described herein further employ antigen-presenting cells (such as dendritic cells or macrophages) that express an ovarian carcinoma polypeptide as provided herein.

Ovarian Carcinoma Polynucleotides

Any polynucleotide that encodes an ovarian carcinoma protein or a
25 portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 45 consecutive nucleotides, that encode a portion of an ovarian carcinoma protein. More preferably, a polynucleotide encodes an immunogenic portion of an ovarian carcinoma
30 protein, such as an ovarian carcinoma antigen. Polynucleotides complementary to any

such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a
5 polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes an ovarian carcinoma protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity
10 of the encoded polypeptide is not diminished, relative to a native ovarian carcinoma protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native ovarian carcinoma protein or
15 a portion thereof.

The percent identity for two polynucleotide or polypeptide sequences may be readily determined by comparing sequences using computer algorithms well known to those of ordinary skill in the art, such as Megalign, using default parameters. Comparisons between two sequences are typically performed by comparing the
20 sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, or 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment of sequences for
25 comparison may be conducted, for example, using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. Preferably, the percentage of sequence identity is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the
30 window may comprise additions or deletions (*i.e.*, gaps) of 20 % or less, usually 5 to 15 %, or 10 to 12%, relative to the reference sequence (which does not contain additions or

deletions). The percent identity may be calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native ovarian carcinoma protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, an ovarian carcinoma polynucleotide may be identified, as described in more detail below, by screening a late passage ovarian tumor expression library with antisera generated against sera of immunocompetent mice after injection of such mice with sera from SCID mice implanted with late passage ovarian tumors. Ovarian carcinoma polynucleotides may also be identified using any of a variety of techniques designed to evaluate differential gene expression. Alternatively, polynucleotides may

be amplified from cDNA prepared from ovarian tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

- 5 An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, an ovarian carcinoma cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for
10 identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

- For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured
15 bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using
20 a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be
25 generated by ligating suitable fragments, using well known techniques.

- Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed
30 using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target

sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding portions of ovarian carcinoma antigens are provided in Figures 1A-1S (SEQ ID NO:1 to 71) and Figures 15A to 15EEE (SEQ ID NO:82 to 310). The sequences provided in Figures 1A-1S appear to be novel. For sequences in Figures 15A-15EEE, database searches revealed matches having substantial identity. These polynucleotides were isolated by serological screening of an ovarian tumor cDNA expression library, using a technique designed to identify secreted tumor antigens. Briefly, a late passage ovarian tumor expression library was prepared from a SCID-derived human ovarian tumor (OV9334) in the vector λ -screen (Novagen). The sera used for screening were obtained by

injecting immunocompetent mice with sera from SCID mice implanted with one late passage ovarian tumors. This technique permits the identification of cDNA molecules that encode immunogenic portions of secreted tumor antigens.

The polynucleotides recited herein, as well as full length polynucleotides comprising such sequences, other portions of such full length polynucleotides, and sequences complementary to all or a portion of such full length molecules, are specifically encompassed by the present invention. It will be apparent to those of ordinary skill in the art that this technique can also be applied to the identification of antigens that are secreted from other types of tumors.

Other nucleic acid sequences of cDNA molecules encoding portions of ovarian carcinoma proteins are provided in Figures 4-9 (SEQ ID NO:75-81), as well as SEQ ID NO:313-384. These sequences were identified by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in an ovarian tumor than in normal ovarian tissue, as determined using a representative assay provided herein). Such screens were performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). SEQ ID NO:311 and 391 provide full length sequences incorporating certain of these nucleic acid sequences.

Any of a variety of well known techniques may be used to evaluate tumor-associated expression of a cDNA. For example, hybridization techniques using labeled polynucleotide probes may be employed. Alternatively, or in addition, amplification techniques such as real-time PCR may be used (*see* Gibson et al., *Genome Research* 6:995-1001, 1996; Heid et al., *Genome Research* 6:986-994, 1996). Real-time PCR is a technique that evaluates the level of PCR product accumulation during amplification. This technique permits quantitative evaluation of mRNA levels in multiple samples. Briefly, mRNA is extracted from tumor and normal tissue and cDNA is prepared using standard techniques. Real-time PCR may be performed, for example, using a Perkin Elmer/Applied Biosystems (Foster City, CA) 7700 Prism instrument. Matching primers and fluorescent probes may be designed for genes of interest using, for example, the primer express program provided by Perkin Elmer/Applied Biosystems

(Foster City, CA). Optimal concentrations of primers and probes may be initially determined by those of ordinary skill in the art, and control (*e.g.*, β -actin) primers and probes may be obtained commercially from, for example, Perkin Elmer/Applied Biosystems (Foster City, CA). To quantitate the amount of specific RNA in a sample, a
5 standard curve is generated alongside using a plasmid containing the gene of interest. Standard curves may be generated using the Ct values determined in the real-time PCR, which are related to the initial cDNA concentration used in the assay. Standard dilutions ranging from 10^{-10} to 10^{-6} copies of the gene of interest are generally sufficient. In addition, a standard curve is generated for the control sequence. This permits
10 standardization of initial RNA content of a tissue sample to the amount of control for comparison purposes.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced
15 using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding an ovarian carcinoma antigen, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain
20 portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo*.

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression.
25 cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells or tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of an ovarian carcinoma protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to
30 open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In* Huber and Carr, *Molecular and Immunologic Approaches*,

Futura Publishing Co. (Mt. Kisco, NY; 1994). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

5 Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-, methyl-, thio- and
10 other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of
15 particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

20 Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For
25 example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (*e.g.*, avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of
30 transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also

be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

Ovarian Carcinoma Polypeptides

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of an ovarian carcinoma protein or a variant thereof, as described herein. As noted above, certain ovarian carcinoma proteins are ovarian carcinoma antigens that are expressed by ovarian tumor cells and react detectably within an immunoassay (such as an ELISA) with antisera generated against serum from an immunodeficient animal implanted with an ovarian tumor. Other ovarian carcinoma proteins are encoded by ovarian carcinoma polynucleotides recited herein. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of an antigen that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of an ovarian carcinoma protein or a variant thereof. Preferred immunogenic portions are encoded by cDNA molecules isolated as described herein. Further immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with ovarian carcinoma protein-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "ovarian carcinoma protein-

specific" if they specifically bind to an ovarian carcinoma protein (*i.e.*, they react with the ovarian carcinoma protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera, antibodies and T cells may be prepared as described herein, and using well known techniques. An immunogenic portion of a native ovarian carcinoma protein is a portion that reacts with such antisera, antibodies and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length protein. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native ovarian carcinoma protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native ovarian carcinoma protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with ovarian carcinoma protein-specific antisera may be enhanced or unchanged, relative to the native ovarian carcinoma protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native ovarian carcinoma protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with ovarian carcinoma protein-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the native polypeptide. Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells

include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available
5 filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic
10 means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is
15 commercially available from suppliers such as Applied BioSystems, Inc. (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises one polypeptide as described herein and a known tumor antigen, such as an ovarian
20 carcinoma protein or a variant of such a protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion
25 partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques,
30 including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused

protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med., 336:86-91, 1997*).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen present cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

Binding Agents

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to an ovarian carcinoma protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to an ovarian carcinoma protein if it reacts at a detectable level (within, for example, an ELISA) with an ovarian carcinoma protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a "complex" is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as ovarian cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to an ovarian carcinoma antigen will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological

samples (*e.g.*, blood, sera, leukophoresis, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the

desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized
5 animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks,
10 colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the
15 yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process
20 in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane,
25 *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides,
30 differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include

methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

5 A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-
10 containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

 Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker
15 group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

 It will be evident to those skilled in the art that a variety of bifunctional
20 or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

25 Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction
30 of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of

derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one
5 embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for
10 attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may
15 also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be
20 formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and
25 immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Also provided herein are anti-idiotypic antibodies that mimic an
30 immunogenic portion of an ovarian carcinoma protein. Such antibodies may be raised against an antibody, or antigen-binding fragment thereof, that specifically binds to an

immunogenic portion of an ovarian carcinoma protein, using well known techniques. Anti-idiotypic antibodies that mimic an immunogenic portion of an ovarian carcinoma protein are those antibodies that bind to an antibody, or antigen-binding fragment thereof, that specifically binds to an immunogenic portion of an ovarian carcinoma protein, as described herein.

T Cells

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for an ovarian carcinoma protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be present within (or isolated from) bone marrow, peripheral blood or a fraction of bone marrow or peripheral blood of a mammal, such as a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human animals, cell lines or cultures.

T cells may be stimulated with an ovarian carcinoma polypeptide, polynucleotide encoding an ovarian carcinoma polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, an ovarian carcinoma polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for an ovarian carcinoma polypeptide if the T cells kill target cells coated with an ovarian carcinoma polypeptide or expressing a gene encoding such a polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be

accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with an ovarian carcinoma polypeptide
5 (200 ng/ml - 100 µg/ml, preferably 100 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells and/or contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., Current
10 Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998). T cells that have been activated in response to an ovarian carcinoma polypeptide, polynucleotide or ovarian carcinoma polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Ovarian carcinoma polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient or a related or
15 unrelated donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to an ovarian carcinoma polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be
20 accomplished in a variety of ways. For example, the T cells can be re-exposed to an ovarian carcinoma polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize an ovarian carcinoma polypeptide. Alternatively, one or more T cells that proliferate in the presence of an ovarian carcinoma polypeptide can be expanded in number by cloning. Methods for
25 cloning cells are well known in the art, and include limiting dilution. Following expansion, the cells may be administered back to the patient as described, for example, by Chang et al., *Crit. Rev. Oncol. Hematol.* 22:213, 1996.

Pharmaceutical Compositions and Vaccines

Within certain aspects, polypeptides, polynucleotides, binding agents
30 and/or immune system cells as described herein may be incorporated into

pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds or cells and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds or cells and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance
5 that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and
10 adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound within the composition or vaccine.

15 A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid
20 expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox
25 virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651;
30 EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al.,

PNAS 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 5 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier 10 will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. 15 For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for 20 example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) 25 and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. 30 Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune

responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ), alum, biodegradable
5 microspheres, monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (*e.g.*, IFN- γ , IL-2 and IL-12) tend to favor the
10 induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6, IL-10 and TNF- β) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly
15 Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type
20 response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; *see* US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). Also preferred is AS-2 (SmithKline Beecham). CpG-containing oligonucleotides (in which the CpG
25 dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the
30 combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO

96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination
5 of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example,
10 oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant
15 level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific
20 immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se*
25 and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic
30 cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to

be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a ovarian carcinoma antigen (or portion or other variant thereof) such that the antigen, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells
5 may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun
10 approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently
15 conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Cancer Therapy

In further aspects of the present invention, the compositions described
20 herein may be used for immunotherapy of cancer, such as ovarian cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a
25 cancer or to treat a patient afflicted with a cancer. Within certain preferred embodiments, a patient is afflicted with ovarian cancer. Such cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration
30 of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immuno response-modifying agents (such as tumor vaccines, bacterial adjuvants and/or
5 cytokines).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host
10 immune system. Examples of effector cells include T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides
15 recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for
20 adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above,
25 immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example,
30 antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system.

Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al.,
5 *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into stem cells taken from a patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

Routes and frequency of administration, as well as dosage, will vary
10 from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration), orally or in the bed of a resected tumor. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are
15 administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level.. Such response can be monitored by measuring
20 the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for
25 pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the
30 active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical

outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to an ovarian carcinoma antigen generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated
5 using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Screens for Identifying Secreted Ovarian Carcinoma Antigens

The present invention provides methods for identifying secreted tumor antigens. Within such methods, tumors are implanted into immunodeficient animals
10 such as SCID mice and maintained for a time sufficient to permit secretion of tumor antigens into serum. In general, tumors may be implanted subcutaneously or within the gonadal fat pad of an immunodeficient animal and maintained for 1-9 months, preferably 1-4 months. Implantation may generally be performed as described in WO 97/18300. The serum containing secreted antigens is then used to prepare antisera in
15 immunocompetent mice, using standard techniques and as described herein. Briefly, 50-100 μ L of sera (pooled from three sets of immunodeficient mice, each set bearing a different SCID-derived human ovarian tumor) may be mixed 1:1 (vol:vol) with an appropriate adjuvant, such as RIBI-MPL or MPL + TDM (Sigma Chemical Co., St. Louis, MO) and injected intraperitoneally into syngeneic immunocompetent animals at
20 monthly intervals for a total of 5 months. Antisera from animals immunized in such a manner may be obtained by drawing blood after the third, fourth and fifth immunizations. The resulting antiserum is generally pre-cleared of *E. coli* and phage antigens and used (generally following dilution, such as 1:200) in a serological expression screen.

25 The library is typically an expression library containing cDNAs from one or more tumors of the type that was implanted into SCID mice. This expression library may be prepared in any suitable vector, such as λ -screen (Novagen). cDNAs that encode a polypeptide that reacts with the antiserum may be identified using standard techniques, and sequenced. Such cDNA molecules may be further characterized to

evaluate expression in tumor and normal tissue, and to evaluate antigen secretion in patients.

The methods provided herein have advantages over other methods for tumor antigen discovery. In particular, all antigens identified by such methods should
5 be secreted or released through necrosis of the tumor cells. Such antigens may be present on the surface of tumor cells for an amount of time sufficient to permit targeting and killing by the immune system, following vaccination.

Methods for Detecting Cancer

In general, a cancer may be detected in a patient based on the presence of
10 one or more ovarian carcinoma proteins and/or polynucleotides encoding such proteins in a biological sample (such as blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as ovarian cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein
15 generally permit detection of the level of protein that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, an ovarian carcinoma-associated sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

20 There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b)
25 detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection
30 reagent that contains a reporter group and specifically binds to the binding

agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length ovarian carcinoma proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports
5 having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.
10 This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a
15 different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically
20 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact
25 time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with ovarian cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve
30 equilibrium may be readily determined by assaying the level of binding that occurs over

a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second
5 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of
10 binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups
15 and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

20 To determine the presence or absence of a cancer, such as ovarian cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with
25 samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985,
30 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity)

that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use
5 ovarian carcinoma polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such ovarian carcinoma protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with an ovarian carcinoma protein in a biological sample.
10 Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with an ovarian carcinoma protein, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated
15 T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with an ovarian carcinoma protein (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of ovarian carcinoma protein to serve as a control. For
20 CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

25 As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding an ovarian carcinoma protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of an ovarian carcinoma protein cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is
30 specific for (*i.e.*, hybridizes to) a polynucleotide encoding the ovarian carcinoma protein. The amplified cDNA is then separated and detected using techniques well

known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding an ovarian carcinoma protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

5 To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding an ovarian carcinoma protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably,
10 oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous
15 nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence provided herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

20 One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample such as a biopsy tissue and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification
25 may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered
30 positive.

In another embodiment, ovarian carcinoma proteins and polynucleotides encoding such proteins may be used as markers for monitoring the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple ovarian carcinoma protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

Diagnostic Kits

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to an ovarian carcinoma protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain

a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding an ovarian carcinoma protein in a biological sample. Such kits generally
5 comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding an ovarian carcinoma protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a
10 polynucleotide encoding an ovarian carcinoma protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

IDENTIFICATION OF REPRESENTATIVE OVARIAN CARCINOMA PROTEIN cDNAs

This Example illustrates the identification of cDNA molecules encoding
5 ovarian carcinoma proteins.

Anti-SCID mouse sera (generated against sera from SCID mice carrying late passage ovarian carcinoma) was pre-cleared of E. coli and phage antigens and used at a 1:200 dilution in a serological expression screen. The library screened was made from a SCID-derived human ovarian tumor (OV9334) using a directional RH oligo(dT)
10 priming cDNA library construction kit and the λ Screen vector (Novagen). A bacteriophage lambda screen was employed. Approximately 400,000 pfu of the amplified OV9334 library were screened.

196 positive clones were isolated. Certain sequences that appear to be novel are provided in Figures 1A-1S and SEQ ID NO:1 to 71. Three complete insert
15 sequences are shown in Figures 2A-2C (SEQ ID NO:72 to 74). Other clones having known sequences are presented in Figures 15A-15EEE (SEQ ID NO:82 to 310). Database searches identified the following sequences that were substantially identical to the sequences presented in Figures 15A-15EEE.

These clones were further characterized using microarray technology to
20 determine mRNA expression levels in a variety of tumor and normal tissues. Such analyses were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions. PCR amplification products were arrayed on slides, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed and fluorescent-labeled cDNA probes
25 were generated. The microarrays were probed with the labeled cDNA probes and the slides were scanned to measure fluorescence intensity. Data was analyzed using Synteni's provided GEMtools software. The results for one clone (13695, also referred to as O8E) are shown in Figure 3.

EXAMPLE 2

IDENTIFICATION OF OVARIAN CARCINOMA cDNAs USING MICROARRAY TECHNOLOGY

This Example illustrates the identification of ovarian carcinoma polynucleotides by PCR subtraction and microarray analysis. Microarrays of cDNAs
5 were analyzed for ovarian tumor-specific expression using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997).

A PCR subtraction was performed using a tester comprising cDNA of
10 four ovarian tumors (three of which were metastatic tumors) and a driver of cDNA from five normal tissues (adrenal gland, lung, pancreas, spleen and brain). cDNA fragments recovered from this subtraction were subjected to DNA microarray analysis where the fragments were PCR amplified, adhered to chips and hybridized with fluorescently labeled probes derived from mRNAs of human ovarian tumors and a variety of normal
15 human tissues. In this analysis, the slides were scanned and the fluorescence intensity was measured, and the data were analyzed using Synteni's GEMtools software. In general, sequences showing at least a 5-fold increase in expression in tumor cells (relative to normal cells) were considered ovarian tumor antigens. The fluorescent results were analyzed and clones that displayed increased expression in ovarian tumors
20 were further characterized by DNA sequencing and database searches to determine the novelty of the sequences.

Using such assays, an ovarian tumor antigen was identified that is a splice fusion between the human T-cell leukemia virus type I oncoprotein TAX (*see* Jin et al., *Cell* 93:81-91, 1998) and an extracellular matrix protein called osteonectin. A
25 splice junction sequence exists at the fusion point. The sequence of this clone is presented in Figure 4 and SEQ ID NO:75. Osteonectin, unspliced and unaltered, was also identified from such assays independently.

Further clones identified by this method are referred to herein as 3f, 6b, 8e, 8h, 12c and 12h. Sequences of these clones are shown in Figures 5 to 9 and SEQ ID
30 NO:76 to 81. Microarray analyses were performed as described above, and are presented in Figures 10 to 14. A full length sequence encompassing clones 3f, 6b, 8e

and 12h was obtained by screening an ovarian tumor (SCID-derived) cDNA library. This 2996 base pair sequence (designated O772P) is presented in SEQ ID NO:311, and the encoded 914 amino acid protein sequence is shown in SEQ ID NO:312. PSORT analysis indicates a Type 1a transmembrane protein localized to the plasma membrane.

- 5 In addition to certain of the sequences described above, this screen identified the following sequences which are described in detail in Table 1:

Table 1

Sequence	Comments
OV4vG11 (SEQ ID NO:313)	human clone 1119D9 on chromosome 20p12
OV4vB11 (SEQ ID NO:314)	human UWGC:y14c094 from chromosome 6p21
OV4vD9 (SEQ ID NO:315)	human clone 1049G16 chromosome 20q12-13.2
OV4vD5 (SEQ ID NO:316)	human KIAA0014 gene
OV4vC2 (SEQ ID NO:317)	human KIAA0084 gene
OV4vF3 (SEQ ID NO:318)	human chromosome 19 cosmid R31167
OV4VC1 (SEQ ID NO:319)	novel
OV4vH3 (SEQ ID NO:320)	novel
OV4vD2 (SEQ ID NO:321)	novel
O815P (SEQ ID NO:322)	novel
OV4vC12 (SEQ ID NO:323)	novel
OV4vA4 (SEQ ID NO:324)	novel
OV4vA3 (SEQ ID NO:325)	novel
OV4v2A5 (SEQ ID NO:326)	novel
O819P (SEQ ID NO:327)	novel
O818P (SEQ ID NO:328)	novel
O817P (SEQ ID NO:329)	novel
O816P (SEQ ID NO:330)	novel
Ov4vC5 (SEQ ID NO:331)	novel
21721 (SEQ ID NO:332)	human lumican
21719 (SEQ ID NO:333)	human retinoic acid-binding protein II
21717 (SEQ ID NO:334)	human26S proteasome ATPase subunit
21654 (SEQ ID NO:335)	human copine I
21627 (SEQ ID NO:336)	human neuron specific gamma-2 enolase

Sequence	Comments
21623 (SEQ ID NO:337)	human geranylgeranyl transferase II
21621 (SEQ ID NO:338)	human cyclin-dependent protein kinase
21616 (SEQ ID NO:339)	human prepro-megakaryocyte potentiating factor
21612 (SEQ ID NO:340)	human UPH1
21558 (SEQ ID NO:341)	human RalGDS-like 2 (RGL2)
21555 (SEQ ID NO:342)	human autoantigen P542
21548 (SEQ ID NO:343)	human actin-related protein (ARP2)
21462 (SEQ ID NO:344)	human huntingtin interacting protein
21441 (SEQ ID NO:345)	human 90K product (tumor associated antigen)
21439 (SEQ ID NO:346)	human guanine nucleotide regulator protein (tim1)
21438 (SEQ ID NO:347)	human Ku autoimmune (p70/p80) antigen
21237 (SEQ ID NO:348)	human S-laminin
21436 (SEQ ID NO:349)	human ribophorin I
21435 (SEQ ID NO:350)	human cytoplasmic chaperonin hTRiC5
21425 (SEQ ID NO:351)	humanEMX2
21423 (SEQ ID NO:352)	human p87/p89 gene
21419 (SEQ ID NO:353)	human HPBR11-7
21252 (SEQ ID NO:354)	human T1-227H
21251 (SEQ ID NO:355)	human cullin I
21247 (SEQ ID NO:356)	kunitz type protease inhibitor (KOP)
21244-1 (SEQ ID NO:357)	human protein tyrosine phosphatase receptor F (PTPRF)
21718 (SEQ ID NO:358)	human LTR repeat
OV2-90 (SEQ ID NO:359)	novel
Human zinc finger (SEQ ID NO:360)	
Human polyA binding protein (SEQ ID NO:361)	
Human pleiotrophin (SEQ ID NO:362)	
Human PAC clone 278C19 (SEQ ID NO:363)	
Human LLRep3 (SEQ ID NO:364)	
Human Kunitz type protease inhib (SEQ ID NO:365)	
Human KIAA0106 gene (SEQ ID NO:366)	
Human keratin (SEQ ID NO:367)	
Human HIV-1TAR (SEQ ID NO:368)	
Human glia derived nexin (SEQ ID NO:369)	

Sequence	Comments
Human fibronectin (SEQ ID NO:370)	
Human ECMproBM40 (SEQ ID NO:371)	
Human collagen (SEQ ID NO:372)	
Human alpha enolase (SEQ ID NO:373)	
Human aldolase (SEQ ID NO:374)	
Human transf growth factor BIG H3 (SEQ ID NO:375)	
Human SPARC osteonectin (SEQ ID NO:376)	
Human SLP1 leucocyte protease (SEQ ID NO:377)	
Human mitochondrial ATP synth (SEQ ID NO:378)	
Human DNA seq clone 461P17 (SEQ ID NO:379)	
Human dbpB pro Y box (SEQ ID NO:380)	
Human 40 kDa keratin (SEQ ID NO:381)	
Human arginosuccinate synth (SEQ ID NO:382)	
Human acidic ribosomal phosphoprotein (SEQ ID NO:383)	
Human colon carcinoma laminin binding pro (SEQ ID NO:384)	

This screen further identified multiple forms of the clone O772P, referred to herein as 21013, 21003 and 21008. PSORT analysis indicates that 21003 (SEQ ID NO:386; translated as SEQ ID NO:389) and 21008 (SEQ ID NO:387; translated as SEQ ID NO:390) represent Type 1a transmembrane protein forms of O772P. 21013 (SEQ ID NO:385; translated as SEQ ID NO:388) appears to be a truncated form of the protein and is predicted by PSORT analysis to be a secreted protein.

Additional sequence analysis resulted in a full length clone for O8E (2627 bp, which agrees with the message size observed by Northern analysis; SEQ ID NO:391). This nucleotide sequence was obtained as follows: the original O8E sequence (OrigO8Econs) was found to overlap by 33 nucleotides with a sequence from an EST clone (IMAGE#1987589). This clone provided 1042 additional nucleotides upstream of the original O8E sequence. The link between the EST and O8E was confirmed by sequencing multiple PCR fragments generated from an ovary primary tumor library using primers to the unique EST and the O8E sequence (ESTxO8EPCR). Full length status was further indicated when anchored PCR from the ovary tumor library gave

several clones (AnchoredPCR cons) that all terminated upstream of the putative start methionine, but failed to yield any additional sequence information. Figure 16 presents a diagram that illustrates the location of each partial sequence within the full length O8E sequence.

- 5 Two protein sequences may be translated from the full length O8E. For "a" (SEQ ID NO:393) begins with a putative start methionine. A second form "b" (SEQ ID NO:392) includes 27 additional upstream residues to the 5' end of the nucleotide sequence.

EXAMPLE 3

- 10 This example discloses the identification and characterization of antibody epitopes recognized by the O8E polyclonal anti-sera.

Rabbit anti-sera was raised against E. coli derived O8E recombinant protein and tested for antibody epitope recognition against 20 or 21 mer peptides that correspond to the O8E amino acid sequence. Peptides spanning amino acid regions 31
15 to 65, 76 to 110, 136 to 200 and 226 to 245 of the full length O8E protein were recognized by an acid eluted peak and/or a salt eluted peak from affinity purified anti-O8E sera. Thus, the corresponding amino acid sequences of the above peptides constitute the antibody epitopes recognized by affinity purified anti-O8E antibodies.

- ELISA analysis of anti-O8E rabbit sera is shown in Figure 23, and ELISA
20 analysis of affinity purified rabbit anti-O8E polyclonal antibody is shown in Figure 24.

For epitope mapping, 20 or 21 mer peptides corresponding to the O8E protein were synthesized. For antibody affinity purification, rabbit anti-O8E sera was run over an O8E-sepharose column, then antibody was eluted with a salt buffer containing 0.5 M NaCl and 20 mM PO₄, followed by an acid elution step using 0.2 M
25 Glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8 and buffer exchanged into phosphate buffered saline (PBS). For enzyme linked immunosorbant assay (ELISA) analysis, O8E peptides and O8E recombinant protein were coated onto 96 well flat bottom plates at 2 µg/ml for 2 hours at room temperature (RT). Plates were then washed 5 times with PBS + 0.1 % Tween 20 and blocked with
30 PBS + 1 % bovine serum albumin (BSA) for 1 hour. Affinity purified anti-O8E antibody, either an acid or salt eluted fraction, was then added to the wells at 1 µg/ml

and incubated at RT for 1 hr. Plates were again washed, followed by the addition of donkey anti-rabbit-Ig-horseradish peroxidase (HRP) antibody for 1 hour at RT. Plates were washed, then developed by the addition of the chromagenic substrate 3, 3', 5, 5'-tetramethylbenzidine (TMB) (described by Bos *et al.*, *J. of Immunoassay* 2:187-204 (1981); available from Sigma (St. Louis, MO)). The reaction was incubated 15 minutes at RT and then stopped by the addition of 1 N H₂SO₄. Plates were read at an optical density of 450 (OD450) in an automated plate reader. The sequences of peptides corresponding to the O8E antibody epitopes are disclosed herein as SEQ ID NO: 394-415. Antibody epitopes recognized by the O8E polyclonal anti-sera are disclosed herein in Figure 17.

EXAMPLE 4

This example discloses IHC analysis of O8E expression in ovarian cancer tissue samples.

For immunohistochemistry studies, paraffin-embedded formalin fixed ovarian cancer tissue was sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody (anti-O8E rabbit affinity purified polyclonal antibody) was added to each section for 25 min followed by a 25 min incubation with an anti-rabbit biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 min incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase system was used along with DAB chromogen to visualize antigen expression. Slides were counterstained with hematoxylin. One (papillary serous carcinoma) of six ovarian cancer tissue sections displayed O8E immunoreactivity. Upon optimization of the staining conditions, 4/5 ovarian cancer samples stained positive using the O8E polyclonal antibody. O8E expression was localized to the plasma membrane.

Six ovarian cancer tissues were analyzed with the anti-O8E rabbit polyclonal antibody. One (papillary serous carcinoma) of six ovarian cancer tissue samples stained positive for O8E expression. O8E expression was localized to the surface membrane.

EXAMPLE 5

This example discloses O8E peptides that are predicted to bind HLA-A2 and to be immunogenic for CD8 T cell responses in humans.

Potential HLA-A2 binding peptides of O8E were predicted by using the
5 full-length open-reading frame (ORF) from O8E and running it through "Episeek," a
program used to predict MHC binding peptides. The program used is based on the
algorithm published by Parker, K.C. *et al.*, *J. Immunol.* 152(1):163-175 (1994)
(incorporated by reference herein in its entirety). 10-mer and 9-mer peptides predicted
to bind HLA-0201 are disclosed herein as SEQ ID NO: 416-435 and SEQ ID NO: 436-
10 455, respectively.

EXAMPLE 6

This example discloses O8E cell surface expression measured by
fluorescence activated cell sorting.

For FACS analysis, cells were washed with ice cold staining buffer
15 (PBS/1% BSA/azide). Next, the cells were incubated for 30 minutes on ice with 10
micrograms/ml of affinity purified rabbit anti-B305D polyclonal antibody. The cells
were washed 3 times with staining buffer and then incubated with a 1:100 dilution of a
goat anti-rabbit Ig (H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice.
Following 3 washes, the cells were resuspended in staining buffer containing prodium
20 iodide, a vital stain that allows for identification of permeable cells, and analyzed by
FACS. O8E surface expression was confirmed on SKBR3 breast cancer cells and
HEK293 cells that stably overexpress the cDNA for O8E. Neither MB415 cells nor
HEK293 cells stably transfected with a control irrelevant plasmid DNA showed surface
expression of O8E (Figures 18 and 19).

25

EXAMPLE 7

This example further evaluates the expression and surface localization of
O8E.

For expression and purification of antigen used for immunization, O8E
expressed in an E. coli recombinant expression system was grown overnight in LB
30 Broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning,

10 ml of the overnight culture was added to 500 ml of 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nanometers) of the culture reached 0.4-0.6 the cells were induced with IPTG (1 mM). 4 hours after induction with IPTG the cells were harvested by centrifugation. The cells
5 were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed. To break open the E. coli cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and
10 pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For protein that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM
15 imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using
20 8M urea, 10 mM tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin such as Hi-Prep Q (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off of the column with an increasing
25 salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. This material was then evaluated for acceptable purity as determined by SDS-PAGE or HPLC, concentration as determined by Lowry assay or Amino Acid Analysis, identity as determined by amino terminal
30 protein sequence, and endotoxin level as determined by the Limulus (LAL) assay. The

proteins were then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

For generation of polyclonal anti-sera, 400 micrograms of each prostate antigen was combined with 100 micrograms of muramyl dipeptide (MDP). Equal
5 volume of Incomplete Freund's Adjuvant (IFA) was added and then mixed. Every four weeks animals were boosted with 100 micrograms of antigen mixed with an equal volume of IFA. Seven days following each boost the animal was bled. Sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

For characterization of polyclonal antisera, 96 well plates were coated
10 with antigen by incubating with 50 microliters (typically 1 microgram) at 4°C for 20 hrs. 250 microliters of BSA blocking buffer was added to the wells and incubated at RT for 2 hrs. Plates were washed 6 times with PBS/0.01% tween. Anti-O8E rabbit sera or affinity purified anti-O8e antibody was diluted in PBS. Fifty microliters of diluted antibody was added to each well and incubated at RT for 30 min. Plates were washed as
15 described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at RT for 30 min. Plates were washed as described above and 100 microliters of TMB microwell Peroxidase Substrate was added to each well. Following a 15 minute incubation in the dark at room temperature the colorimetric reaction was stopped with 100 microliters of 1N H₂SO₄ and read
20 immediately at 450 nm. All polyclonal antibodies showed immunoreactivity to the O8E antigen.

For recombinant expression in mammalian HEK293 cells, full length O8E cDNA was subcloned into the mammalian expression vectors pcDNA3.1+ and pCEP4 (Invitrogen) which were modified to contain His and FLAG epitope tags,
25 respectively. These constructs were transfected into HEK293 cells (ATCC) using Fugene 6 reagent (Roche). Briefly, HEK293 cells were plated at a density of 100,000 cells/ml in DMEM (Gibco) containing 10% FBS (Hyclone) and grown overnight. The following day, 2 ul of Fugene6 was added to 100 ul of DMEM containing no FBS and incubated for 15 minutes at room temperature. The Fugene6/DMEM mixture was then
30 added to 1ug of O8E/pCEP4 or O8E/pcDNA3.1 plasmid DNA and incubated for 15 minutes at room temperature. The Fugene/DNA mix was then added to the HEK293

cells and incubated for 48-72 hrs at 37°C with 7% CO₂. Cells were rinsed with PBS then collected and pelleted by centrifugation. For Western blot analysis, whole cell lysates were generated by incubating the cells in Triton-X100 containing lysis buffer for 30 minutes on ice. Lysates were then cleared by centrifugation at 10,000rpm for 5 minutes at 4 C. Samples were diluted with SDS-PAGE loading buffer containing beta-mercaptoethanol, then boiled for 10 minutes prior to loading the SDS-PAGE gel. Protein was transferred to nitrocellulose and probed using anti-O8E rabbit polyclonal sera #2333L at a dilution of 1:750. The blot was revealed with a goat anti-rabbit Ig coupled to HRP followed by incubation in ECL substrate.

10 For FACS analysis, cells were washed further with ice cold staining buffer (PBS+1%BSA+Azide). Next, the cells were incubated for 30 minutes on ice with 10ug/ml of Protein A purified anti-O8E polyclonal sera. The cells were washed 3 times with staining buffer and then incubated with a 1:100 dilution of a goat anti-rabbit Ig(H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice. Following 3 washes, the cells were resuspended in staining buffer containing Propidium Iodide (PI), a vital stain that allows for the identification of permeable cells, and analyzed by FACS.

From these experiments, the results of which are illustrated in Figures 20-21, O8E expression was detected on the surface of transfected HEK293 cells and SKBR3 cells by FACS analysis using rabbit anti-O8E sera. Expression was also detected in transfected HEK293 cell lysates by Western blot analysis (Figure 22).

EXAMPLE 8

GENERATION AND CHARACTERIZATION OF ANTI-O8E MABS.

Mouse monoclonal antibodies were raised against E. coli derived O8E proteins as follows. A/J mice were immunized intraperitoneally (IP) with Complete Freund's Adjuvant (CFA) containing 50 µg recombinant O8E, followed by a subsequent IP boost with Incomplete Freund's Adjuvant (IFA) containing 10µg recombinant O8E protein. Three days prior to removal of the spleens, the mice were immunized intravenously with approximately 50µg of soluble O8E recombinant protein. The spleen of a mouse with a positive titer to O8E was removed, and a single-cell suspension made and used for fusion to SP2/0 myeloma cells to generate B cell

hybridomas. The supernatants from the hybrid clones were tested by ELISA for specificity to recombinant O8E, and epitope mapped using peptides that spanned the entire O8E sequence. The mAbs were also tested by flow cytometry for their ability to detect O8E on the surface of cells stably transfected with O8E and on the surface of a breast tumor cell line.

For ELISA analysis, 96 well plates were coated with either recombinant O8E protein or overlapping 20-mer peptides spanning the entire O8E molecule at a concentration of either 1-2 μ g/ml or 10 μ g/ml, respectively. After coating, the plates were washed 5 times with washing buffer (PBS + 0.1% Tween-20) and blocked with PBS containing 0.5% BSA, 0.4% Tween-20. Hybrid supernatants or purified mAbs were then added and the plates incubated for 60 minutes at room temperature. The plates were washed 5 times with washing buffer and the secondary antibody, donkey-anti mouse Ig linked to horseradish peroxidase (HRP)(Jackson ImmunoResearch), was added for 60 minutes. The plates were again washed 5 times in washing buffer, followed by the addition of the peroxidase substrate. Of the hybridoma clones generated, 15 secreted mAbs that recognized the entire O8E protein. Epitope mapping revealed that of these 15 clones, 14 secreted mAbs that recognized the O8E amino acid residues 61-80 and one clone secreted a mAb that recognized amino acid residues 151-170.

For flow cytometric analysis, HEK293 cells which had been stably transfected with O8E and SKBR3 cells which express O8E mRNA, were harvested and washed in flow staining buffer (PBS+1%BSA+Azide). The cells were incubated with the supernatant from the mAb hybrids for 30 minutes on ice followed by 3 washes with staining buffer. The cells were incubated with goat-anti mouse Ig-FITC for 30 minutes on ice, followed by three washes with staining buffer before being resuspended in wash buffer containing propidium iodide. Flow cytometric analysis revealed that 15/15 mAbs were able to detect O8E protein expressed on the surface of O8E-transfected HEK293 cells. 6/6 mAbs tested on SKBR3 cells were able to recognize surface expressed O8E.

EXAMPLE 9

EXTENDED DNA AND PROTEIN SEQUENCE ANALYSIS OF SEQUENCE O772P

A full-length sequence encompassing clones 3f, 6b, 8e, and 12 was obtained by screening an ovarian tumor (SCID-derived) cDNA library described in detail in Example 2. This 2996 base pair sequence, designated O772P, is presented in SEQ ID NO: 311, and the encoded 914 amino acid protein sequence is shown in SEQ ID NO: 312. The DNA sequence O772P was searched against public databases including Genbank and showed a significant hit to Genbank Accession number AK024365 (SEQ ID NO: 457). This Genbank sequence was found to be 3557 base pairs in length and encodes a protein 1156 amino acids in length (SEQ ID NO: 459). A truncated version of this sequence, residues 25-3471, in which residue 25 corresponds to the first ATG initiation codon in the Genbank sequence, (SEQ ID NO: 456), encodes a protein that is 1148 amino acids in length (SEQ ID NO: 458). The published DNA sequence (SEQ ID NO: 457) differs from O772P in that it has a 5 base pair insertion corresponding to bases 958-962 of SEQ ID NO: 457. This insertion results in a frame shift such that SEQ ID NO: 457 encodes an additional N-terminal protein sequence relative to O772P (SEQ ID NO: 312). In addition, O772P encodes a unique N-terminal portion contained in residues 1-79 (SEQ ID NO: 460). The N-terminal portion of SEQ ID NO: 456, residues 1-313, also contains unique sequence and is listed as SEQ ID NO: 461.

EXAMPLE 10

THE GENERATION OF POLYCLONAL ANTIBODIES FOR IMMUNOHISTOCHEMISTRY
AND FLOW CYTOMETRIC ANALYSIS OF THE CELL ASSOCIATED EXPRESSION
PATTERN OF MOLECULE O772P

The O772P molecule was identified in Examples 2 and 9 of this application. To evaluate the subcellular localization and specificity of antigen expression in various tissues, polyclonal antibodies were generated against O772P. To produce these antibodies, O772P-1 (amino acids 44-772 of SEQ ID NO:312) and O772P-2 (477-914 of SEQ ID NO:312) were expressed in an E. coli recombinant expression system and grown overnight at 37°C in LB Broth. The following day, 10ml

of the overnight culture was added to 500ml of 2xYT containing the appropriate antibiotics. When the optical density of the cultures (560 nanometers) reached 0.4-0.6 the cells were induced with IPTG. Following induction, the cells were harvested, washed, lysed and run through a French Press at a pressure of 16000 psi. The cells were
5 then centrifuged and the pellet checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localize to the cell pellet, the pellet was resuspended in 10mM Tris, pH 8.0, 1% CHAPS and the inclusion body pellet washed and centrifuged. The washed inclusion body was solubilized with either 8M urea or 6M guanidine HCL containing 10mM Tris, pH 8.0, plus 10mM imidazole. The solubilized
10 protein was then added to 5ml of nickel-chelate resin (Qiagen) and incubated for 45 minutes at room temperature.

Following the incubation, the resin and protein mixture was poured through a column and the flow through collected. The column was washed with 10-20 column volumes of buffer and the antigen eluted using 8M urea, 10mM Tris, pH 8.0,
15 and 300 mM imidazole and collected in 3ml fractions. SDS-PAGE was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin was equilibrated with the appropriate buffer and the pooled fractions were loaded onto the column. Each antigen was eluted from the column with an increasing salt gradient. Fractions were collected and analyzed by a SDS-PAGE to
20 determine which fractions from the column to pool. The pooled fractions were dialyzed against 10mM Tris, pH 8.0, and the resulting protein was submitted for quality control for final release. The release criteria were: (a) purity as determined by SDS-PAGE or HPLC, (b) concentration as determined by Lowry assay or Amino Acid Analysis, (c) identity as determined by amino terminal protein, and (d) endotoxin levels as
25 determined by the Limulus (LAL) assay. The proteins were then filtered through a 0.22 μ M filter and frozen until needed for immunizations.

To generate polyclonal antisera, 400 μ g of O772P-1 or O772P-2 was combined with 100 μ g of muramyl dipeptide (MDP). The rabbits were immunized every 4 weeks with 100 μ g of antigen mixed with an equal volume of Incomplete Freund's
30 Adjuvant (IFA). Seven days following each boost, the animals were bled and sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

To characterize the antisera, 96 well plates were coated with antigen followed by blocking with BSA. Rabbit sera was diluted in PBS and added to each well. The plates were then washed, and goat anti-rabbit horseradish peroxidase (HRP). The plates were again washed and TMB microwell Peroxidase Substrate was added.

5 Following this incubation, the colormetric reaction was stopped and the plates read immediately at 450nm. All polyclonal antibodies showed immunoreactivity to the appropriate antigen.

Immunohistochemistry analysis of O772P expression was performed on paraffin-embedded formalin fixed tissue. O772P was found to be expressed in normal

10 ovary and ovarian tumor, but not in normal heart, kidney, colon, lung or liver. Additionally, immunohistochemistry and flow cytometric analysis indicates that O772P is a plasma membrane-associated molecule. O772P contains 1 plasma transmembrane domain predicted to be encoded by amino acids 859-880. The N-terminus of O772P is extracellular and is encoded by amino acids 1-859, while the C-terminus is intracellular.

15 Sequence analysis shows that there are 17 potential N-linked glycosylation sites.

EXAMPLE 11

O772P IS EXPRESSED ON THE SURFACE OF PRIMARY OVARIAN TUMOR CELLS

For recombinant expression in mammalian cells, the O772P-21008 (SEQ ID NO:387) and O772P full length cDNA (SEQ ID NO:311 encoding the protein of

20 SEQ ID NO:312) were subcloned into mammalian expression vectors pBIB or pCEP4 respectively. These constructs were transfected into HEK293 cells using Fugene 6 (Roche). The HEK cells were then plated at a density of 100,000 cells/ml in DMEM containing fetal bovine serum (FBS) and grown overnight. The following day, 2 μ l of Fugene 6 was added to 100 μ l of DMEM, which contained no FBS, and incubated for 15

25 minutes at room temperature. The Fugene 6/DMEM mixture was then added to 1 μ g of O772P/pBIB or O772P/pCEP4 plasmid DNA and incubated for an additional 15 minutes at room temperature. The Fugene 6/DNA mix was then added to the HEK293 cells and incubated for 48-72 hours at 37°C with 7% CO₂. The cells were rinsed and pelleted by centrifugation.

For Western Blot analysis, whole cell lysates were generated by incubating the cells in lysis buffer followed by clarification by centrifugation. The samples were diluted and run on SDS-PAGE. The gel was then transferred to nitrocellulose and probed using purified anti-O772P-2 rabbit polyclonal antibody. The blot was revealed with a goat anti-rabbit Ig coupled to HRP followed by incubation in ECL substrate. Western Blot analysis revealed that O772P-21008 could be detected in HEK293 cells that had been transfected with O772P.

To determine the cell expression profile of O772P in cells, primary ovarian tumor cells were grown in SCID mice. The cells were retrieved from the mice and analyzed by flow cytometry. Briefly, cells washed in cold staining buffer containing PBS, 1% BSA, and Na Azide. The cells were incubated for 30 minutes with 10µg/ml of purified anti-O772P-1 and O772P-2 polyclonal sera. Following this incubation, the cells were washed three times in staining buffer and incubated with goat anti-rabbit Ig (H+L) conjugated to FITC (Southern Biotechnology). The cells were washed and resuspended in staining buffer containing Propidium Iodide (PI), a vital stain that identifies non-viable cells. The cells were then analyzed using Fluorescence Activated Cell Sorting (FACS). FACS analysis revealed that O772P was present on the cells surface. Surface expression of O772P on tumor cells allows for immune targeting by therapeutic antibodies.

20

EXAMPLE 12

FUNCTIONAL CHARACTERIZATION OF ANTI-O8E MONOCLONAL ANTIBODIES

Mouse monoclonal antibodies (mAb) raised against E. coli derived O8E, as described in Example 8, were tested for their ability to promote O8E antigen internalization. Internalization of the antibody was determined using an in vitro cytotoxicity assay. Briefly, HEK293 and O8E/HEK transfected cells were plated into 96 well plates containing DME plus 10% heat-inactivated FBS in the presence of 50ng/well of purified anti-O8E or control antibodies. The isotype of the anti-O8E mAbs are as follows: 11A6-IgG1/kappa, 15C6-IgG2b/kappa, 18A8-IgG2b/kappa, and 14F1-IgG2a/kappa. W6/32 is a pan anti-human MHC class I mouse monoclonal antibody that serves as a positive control, and two irrelevant mAbs, Ir-Pharm and Ir-

30

Crxα were included as negative controls. Following incubation with the O8E specific antibodies or the relevant controls antibodies, the mAb-zap, a goat anti-mouse Ig-saporin conjugated secondary antibody (Advanced Targeting Systems) was added at a concentration of 100ng/ml to half of the wells, and the plates were incubated for 48 to 5 72 hours at 37°C in a 7% CO₂ incubator. This assay takes advantage of the toxic nature of saporin, a ribozyme inactivating protein, which when internalized has a cytotoxic effect. Following incubation with the mAb-zap, internalization was quantitated by the addition of MTS reagent, followed by reading the OD490 of the plate on a microplate ELISA reader. Figure 25 depicts the results from these assays. The top panel represents 10 HEK cells that have not been transfected with O8E and therefore O8E antibody should not bind and be internalized. Levels of proliferation were the same in all samples whether they were incubated with or without the mAb-zap, with the exception of the positive control Ab, W6/32. The lower panel represents cells that have been transfected with O8E and therefore should bind O8E specific antibodies. Antibodies from the 15 hybridomas 11H6, 14F1, and 15C6, which recognize the amino acids 61-80 of O8E were able to promote internalization of the O8E surface protein as measured by decreased levels of proliferation due to the toxic nature of the mAb-zap (See Figure 25). The antibody generated by the hybridoma 18A8, which recognizes amino acids 151-170 of O8E, was unable to promote internalization as determined by normal levels of 20 proliferation either in the absence or presence of the mAb-zap.

EXAMPLE 13

CHARACTERIZATION OF THE OVARIAN TUMOR ANTIGEN, O772P

The cDNA and protein sequences for multiple forms of the ovarian tumor antigen O772P have been described in the above (e.g., Examples 2 and 9). A 25 Genbank search indicated that O772P has a high degree of similarity with FLJ14303 (Accession # AK024365; SEQ ID NO:457 and 463). Protein sequences corresponding to O772P and FLJ14303 are disclosed in SEQ ID NO:478 and 479, respectively. FLJ14303 was identical to the majority of O772P, with much of the 3'-end showing 100% homology. However, the 5'-end of FLJ14303 was found to extend further 5' than 30 O772P. In addition, FLJ14303 contained a 5 bp insert (SEQ ID NO:457) resulting in a

frame shift of the amino-terminus protein sequence such that FLJ14303 utilizes a different starting methionine than O772P and therefore encodes a different protein. This insertion was present in the genomic sequence and seen in all EST clones that showed identity to this region, suggesting that FLJ14303 (SEQ ID NO:457) represents a splice variant of O772P, with an ORF that contains an extended and different amino-terminus. The additional 5'-nucleotide sequence included repeat sequences that were identified during the genomic mapping of O772P. The 5'-end of O772P and the corresponding region of FLJ14303 showed between 90-100% homology. Taken together, this suggests that O772P and FLJ14303 are different splice variants of the same gene, with different unique repeat sequences being spliced into the 5'-end of the gene.

The identification of an additional ten or more repeat sequences within the same region of chromosome 19, indicates that there may be many forms of O772P, each with a different 5'-end, due to differential splicing of different repeat sequences. Northern blot analysis of O772P demonstrated multiple O772P-hybridizing transcripts of different sizes, some in excess 10kb.

Upon further analysis, 13 additional O772P-related sequences were identified, the cDNA and amino acid sequences of which are described in Table 2.

Table 2

SEQ ID NO:	Description	Transmembrane Domains
464	LS #1043400.1 (cDNA)	nd
465	LS #1043400.10 (cDNA)	0
466	LS #1043400.11 (cDNA)	2
467	LS #1043400.12 (cDNA)	2
468	LS #1043400.2 (cDNA)	nd
469	LS #1043400.3 (cDNA)	
470	LS #1043400.5 (cDNA)	nd
471	LS #1043400.8 (cDNA)	1
472	LS #1043400.9 (cDNA)	0

473	LS #1043400.6 (cDNA)	nd
474	LS #1043400.7 (cDNA)	nd
475	LS #1043400.4 (cDNA)	nd
476	LS #1397610.1 (cDNA)	0
477	1043400.10 Novel 5' (cDNA)	-
480	LS #1043400.9 (amino acid)	-
481	LS #1043400.8B (amino acid) Contains a transmembrane domain	-
482	LS #1043400.8A (amino acid)	-
483	LS #1043400.12 (amino acid) Contains a transmembrane domain	-
484	LS #1043400.11B (amino acid) Contains a transmembrane domain	-
485	LS #1043400.11A (amino acid)	-
486	LS #1043400.10 (amino acid)	-
487	LS #1043400.1 (amino acid)	-

nd=not determined

Initially it appeared that these sequences represented overlapping and/or discrete sequences of O772P splice forms that were capable of encoding polypeptides unique to the specific splice forms of O772P. However, nucleotide alignment of these sequences failed to identify any identical regions within the repeat elements. This indicates that the sequences may represent different specific regions of a single O772P gene, one that contains 16 or more repeat domains, all of which form a single linear transcript. The 5'-end of sequence LS #1043400.10 (Table 2; SEQ ID NO:465) is unique to both O772P and FLJ14303 and contains no repeat elements, indicating that this sequence may represent the 5'-end of O772P.

Previously, transmembrane prediction analysis had indicated that O772P contained between 1 and 3 transmembrane spanning domains. This was verified by the

use of immunohistochemistry and flow cytometry, which demonstrated the existence of a plasma membrane-associated molecule representing O772P. However, immunohistochemistry also indicated the presence of secreted form(s) of O772P, possibly resulting from an alternative splice form of O772P or from a post-translational
5 cleavage event. Analysis of several of the sequences presented in Table 2 showed that sequences 1043400B.12, 1043400.8B, and 1043400.11B all contained transmembrane regions, while 1043400.8A, 1043400.10, 1043400.1, 1043400.11A, and 1043400.9 were all lacking transmembrane sequences, suggesting that these proteins may be secreted.

10 Analysis indicates a part of O772P is expressed and/or retained on the plasma membrane, making O772P an attractive target for directing specific immunotherapies, e.g., therapeutic antibodies, against this protein. The predicted extracellular domain of O772P is disclosed in SEQ ID NO:489 and secretion of O772P is likely to occur as a result of a cleavage event within the sequence:

15 SLVEQVFLDKTLNASFWLGGSTYQLVDIHVTEMESSVYQP.

Proteolytic cleavage is most likely to occur at the Lysine (K) at position 10 of SEQ ID NO:489. The extracellular, transmembrane, and cytoplasmic regions of O772P are all disclosed in SEQ ID NO:488:

Extracellular:

20 SLVEQVFLDKTLNASFWLGGSTYQLVDIHVTEMESSVYQPTSSSS
TQHFYLNFTITNLPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQ
VSTFRSVPNRHHTGVDSL CNFSPLARRVDRVAIYEEFLRMTRNGTQLQNFTLDR
SSVLVDGYFPNRNEPLTGNSDLPF

Transmembrane:

25 WAVILIGLAGLLGLITCLICGVLVTT

Cytoplasmic:

RRRKKEGEYNVQQQCPGYYSHLDEDLQ

EXAMPLE 14

IMMUNOHISTOCHEMISTRY (IHC) ANALYSIS OF O8E EXPRESSION IN OVARIAN CANCER
AND NORMAL TISSUES

In order to determine which tissues express the ovarian cancer antigen O8E, IHC analysis was performed on a diverse range of tissue sections using both polyclonal and monoclonal antibodies specific for O8E. The generation of O8E specific polyclonal antibodies is described in detail in Example 8. The monoclonal antibodies used for staining were 11A6 and 14F1, both of which are specific for amino acids 61-80 of O8E and 18A8, which recognizes amino acids 151-170 of O8E (see Example 12 for details on generation).

To perform staining, tissue samples were fixed in formalin solution for 12-24 hours and embedded in paraffin before being sliced into 8 micron sections. Steam heat induced epitope retrieval (SHEIR) in 0.1M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody was then added to each section for 25 minutes followed by 25 minutes of incubation with either anti-rabbit or anti-mouse biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize the antigen expression. Slides were counterstained with hematoxylin to visualize the cell nuclei.

Results using rabbit affinity purified polyclonal antibody to O8E (a.a. 29-283; for details on the generation of this Ab, see Example 3) are presented in Table 3. Results using the three monoclonal antibodies are presented in Table 4.

Table 3

Immunohistochemistry analysis of O8E using polyclonal antibodies

Tissue	O8E Expression
Ovarian Cancer	Positive
Breast Cancer	Positive

Normal Ovary	Positive
Normal Breast	Positive
Blood Vessel	Positive
Kidney	Negative
Lung	Negative
Colon	Negative
Liver	Negative
Heart	Negative

Table 4

Immunohistochemistry analysis of O8E using monoclonal antibodies

Normal Tissue	11A6		18A8		14F1	
	Endothelia	Epithelial	Endothelial	Epithelial	Endothelial	Epithelial
	1					
Skin	2	2	0	0	1	1
Skin	1	1	0	0	1	1
Breast	0	1	n/a	n/a	1	1
Colon	0	0	0	0	0	0
Jejunum	0	0	0	0	0	0
Colon	0	0	0	0	0	0
Colon	0	0	0	0	0	0
Ovary	0	0	0	0	1	0
Colon	0	0	0	0	0	1
Liver	0	0	0	0	1	2
Skin	0	0	0	0	1	0
Duodenum and Pancreas	0	0	0	0	0	0
Appendix	0	0	0	0	0	0
Ileum	0	0	0	0	0	0

0=no staining, 1=light staining, 2=moderate staining, n/a=not available

EXAMPLE 15

EPIOTOPE MAPPING OF O772P POLYCLONAL ANTIBODIES

To perform epitope mapping of O772P, peptides were generated, the sequences of which were derived from the sequence of O772P. These peptides were 15 mers that overlapped by 5 amino acids and were generated via chemical synthesis on membrane supports. The peptides were covalently bound to Whatman 50 cellulose support by their C-terminus with the N-terminus unbound. In order to determine epitope specificity, the membranes were wet with 100% ethanol for 1 minute, and then blocked for 16 hours in TBS/Tween/Triton buffer (50mM Tris, 137 mM NaCl, 2.7 mM KCl, 0.5% BSA, 0.05% Tween 20, 0.05% Triton X-100, pH 7.5). The peptides were then probed with 2 O772P specific antibodies, O772P-1 (amino acids 44-772 of SEQ ID NO:312) and O772P-2 (477-914 of SEQ ID NO:312; see Example 10 for details of antibody generation), as well as irrelevant rabbit antibodies for controls. The antibodies were diluted to 1µg/ml and incubated with the membranes for 2 hours at room temperature. The membranes were then washed for 30 minutes in TBS/Tween/Triton buffer, prior to being incubated with a 1:10,000 dilution of HRP-conjugated anti-rabbit secondary antibody for 2 hours. The membranes were again washed for 30 minutes in TBS/Tween/Triton and anti-peptide reactivity was visualized using ECL. Specific epitope binding specificity for each of the O772P-polyclonal antibodies is described in Table 5.

Table 5

SEQ ID NO:	Peptide #	Anti-O772P1	Anti-O772P2	Peptide Sequence
490	2	***	-	TCGMRRTCSTLAPGS
491	6	*	*/-	CRLTLLRPEKDGTAT
492	7	*	-	DGTATGVDAICTHHP
493	8	-	-	CTHHPDPKSPRLDRE
494	9	***	***	RLDREQLYWELSQLT
495	11	*/-	-	LGPYALDNDSLFVNG
496	13	****	-	SVSTTSTPGTPTYVL
497	22	-	-	LRPEKDGEATGVDAI
498	24	**	*/-	DPTGPGLDREQLYLE
499	27	*/-	-	LDRDSLYVNGFTHRS
500	40	*/-	-	GPYSLDKDSLYLNGY
501	41	-	-	YLNGYNEPGPDEPPT
502	47	***	***	ATFNSTEGVLQHLLR

503	50	-	***	QLISLRPEKDGAATG
504	51	-	**	GAATGVDTTCTYHPD
505	52	-	*/-	TYHPDPVGPGLDIQQ
506	53	-	*	LDIQQLYWELSQLTH
507	58	-	*	HIVNWNLSNPDPTSS
508	59	-	*	DPTSSEYITLLRDIQ
509	60	-	*	LRDIQDKVTTLYKGS
510	61	-	***	LYKGSQQLHDTFRFCL
511	71	-	**	DKAQPGTTNYQRNKR

*= relative reactive level, -; no binding, ***; maximal binding

EXAMPLE 16

IDENTIFICATION OF A NOVEL N-TERMINAL REPEAT STRUCTURE ASSOCIATED WITH O772P

- 5 Various O772P cDNA and protein forms have been identified and characterized as detailed above (e.g., Examples 1, 2, 9, and 14). Importantly, O772P RNA and protein have been demonstrated to be over-expressed in ovarian cancer tissue relative to normal tissues and thus represents an attractive target for ovarian cancer diagnostic and therapeutic applications.
- 10 Using bioinformatic analysis of open reading frames (ORFs) from genomic nucleotide sequence identified previously as having homology with O772P, multiple nucleotide repeat sequences were identified in the 5' region of the gene encoding the O772P protein. A number of these repeat sequences were confirmed by RT-PCR using primers specific for the individual repeats. Fragments which contained
- 15 multiple repeats were amplified from cDNA, thus confirming the presence of specific repeats and allowing an order of these repeats to be established.

Unexpectedly, when various sets of O772P sequences derived from different database and laboratory sources were analyzed, at least 20 different repeat structures, each having substantial levels of identity with each other (see Table 6), were

20 identified in the 5' region of the O772P gene and the corresponding N-terminal region of the O772P protein. Each repeat comprises a contiguous open reading frame encoding a polypeptide unit that is capable of being spliced to one or more other repeats such that concatomers of the repeats are formed in differing numbers and orders. Interestingly, other molecules have been described in the scientific literature that have repeating

25 structural domains analogous to those described herein for O772P. For example, the

mucin family of proteins, which are the major glycoprotein component of the mucous which coats the surfaces of cells lining the respiratory, digestive and urogenital tracts, have been shown to be composed of tandemly repeated sequences that vary in number, length and amino acid sequence from one mucin to another (Perez-Vilar and Hill, *J. Biol. Chem.* 274(45):31751-31754, 1999).

The various identified repeat structures set forth herein are expected to give rise to multiple forms of O772P, most likely by alternative splicing. The cDNA sequences of the identified repeats are set forth in SEQ ID NOs:513-540, 542-546, and 548-567. The encoded amino acid sequences of the repeats are set forth in SEQ ID NOs:574-593. In many instances these amino acid sequences represent consensus sequences that were derived from the alignment of more than one experimentally derived sequence.

Each of these splice forms is capable of encoding a unique O772P protein with multiple repeat domains attached to a constant carboxy terminal protein portion of O772P that contains a trans membrane region. The cDNA sequence of the O772P constant region is set forth in SEQ ID NO:568 and the encoded amino acid sequence is set forth in SEQ ID NO:594.

All of the available O772P sequences that were obtained were broken down into their identifiable repeats and these sequences were compared using the Clustal method with weighted residue weight table (MegAlign software within DNASTAR sequence analysis package) to identify the relationship between the repeat sequences. Using this information, the ordering data provided by the RT-PCR, and sequence alignments (automatic and manual) using SeqMan (DNASTAR), one illustrative consensus full length O772P contig was identified comprising 20 distinct repeat units. The cDNA for this O772P cDNA contig is set forth in SEQ ID NO:569 and the encoded amino acid sequence is set forth in SEQ ID NO:595. This form of the O772P protein includes the following consensus repeat structures in the following order:

SEQ ID NO:572- SEQ ID NO:574- SEQ ID NO:575-SEQ ID NO:576-
SEQ ID NO:577- SEQ ID NO:578- SEQ ID NO:579- SEQ ID NO:580- SEQ ID
NO:581- SEQ ID NO:582- SEQ ID NO:583- SEQ ID NO:584- SEQ ID NO:585- SEQ

ID NO:586- SEQ ID NO:587- SEQ ID NO:588- SEQ ID NO:589- SEQ ID NO:590-
SEQ ID NO:591- SEQ ID NO:592- SEQ ID NO:593.

SEQ ID NO:595, therefore, represents one illustrative full-length
consensus sequence for the O772P protein. As discussed above, however, based on
5 current knowledge of this protein and based upon scientific literature describing
proteins containing analogous repeating structures, many other forms of O772P are
expected to exist with either more or less repeats. In addition, many forms of O772P
are expected to have differing arrangements, e.g., different orders, of these N-terminal
repeat structures. The existence of multiple forms of O772P having differing numbers
10 of repeats is supported by Northern analysis of O772P. In this study, Northern
hybridization of a O772P-specific probe resulted in a smear of multiple O772P-
hybridizing transcripts, some in excess 10kb.

Thus, the variable repeat region of the O772 protein can be illustratively
represented by the structure $X_n - Y$, wherein X comprises a repeat structure having at
15 least 50% identity with the consensus repeat sequence set forth in SEQ ID NO:596; n is
the number of repeats present in the protein and is expected to typically be a integer
from 1 to about 35; Y comprise the O772P constant region sequence set forth in SEQ
ID NO:594 or sequences having at least 80% identity with SEQ ID NO:594. Each X
present in the X_n repeat region of the O772 molecule is different.

20 To determine the consensus sequences of each of the 20 repeat regions,
sequences that were experimentally determined for a discrete repeat region were aligned
and a consensus sequence determined. In addition to determining the consensus
sequences for individual repeat regions, a consensus repeat sequence was also
determined. This sequence was obtained by aligning the 20 individual consensus
25 sequences. Variability of the repeats was determined by aligning the consensus amino
acid sequences from each of the individual repeat regions with the over all repeat
consensus sequence. Identity data is presented in Table 6.

Table 6

Percent identities of Repeat Sequences with Reference to the Consensus Repeat Sequence

Repeat Number (amino acid)	SEQ ID NO:	Percent Identity to Consensus Repeat Sequence
2	574	88
3	575	84
4	576	88
5	577	89
6	578	93
7	579	90
8	580	91
9	581	88
10	582	85
11	583	86
12	584	87
13	585	87
14	586	89
15	587	89
16	588	89
17	589	83
18	590	84
19	591	83
20	592	57
21	593	68

5 From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration,

various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An O772P polypeptide having the structure:
 X_n -Y
wherein X comprises a sequence having at least 50% identity with the consensus O772P repeat sequence set forth in SEQ ID NO: 596;
Y comprises a sequence having at least 80% identity with the O772P constant region sequence set forth in SEQ ID NO: 594;
n is an integer from 1 to 35;
wherein each X present in said polypeptide is different.
2. The polypeptide of claim 1, wherein X comprises a sequence selected from the group consisting of any one of SEQ ID NOs: 574-593.
3. The polypeptide of claim 1, wherein Y comprises the sequence set forth in SEQ ID NO: 594.
4. The polypeptide of claim 1, wherein n is an integer from 15 to 25.
5. The polypeptide of claim 1, wherein n is 20.
6. The polypeptide of claim 1, wherein said polypeptide comprises SEQ ID NO: 595.
7. The polypeptide of claim 1, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.
8. An O772P polypeptide having the structure:
 X_n -Y

wherein X comprises an O772P repeat sequence selected from the group consisting of any one of SEQ ID NOs: 574-593;

Y comprises a sequence having at least 90% identity with the O772P constant region sequence set forth in SEQ ID NO: 594;

n is an integer from 15 to 25;

wherein each X present in said polypeptide is different.

9. The polypeptide of claim 8, wherein n is 20.
10. The polypeptide of claim 8, wherein said polypeptide comprises SEQ ID NO: 595.
11. The polypeptide of claim 8, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.
12. An O772P polypeptide having the structure:
 X_n-Y
wherein n is 20 and X comprises the following O772P repeat sequences:
SEQ ID NO: 574 - SEQ ID NO: 575 - SEQ ID NO: 576 - SEQ ID NO: 577 - SEQ ID NO: 578 - SEQ ID NO: 579 - SEQ ID NO: 580 - SEQ ID NO: 581 - SEQ ID NO: 582 - SEQ ID NO: 583 - SEQ ID NO: 584 - SEQ ID NO: 585 - SEQ ID NO: 586 - SEQ ID NO: 587 - SEQ ID NO: 588 - SEQ ID NO: 589 - SEQ ID NO: 590 - SEQ ID NO: 591 - SEQ ID NO: 592 - SEQ ID NO: 593; and
Y comprises the sequence set forth in SEQ ID NO: 594.
13. The polypeptide of claim 12, wherein said polypeptide comprises SEQ ID NO: 595.
14. The polypeptide of claim 12, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.

15. An O772P polynucleotide having the structure:

X_n -Y

wherein X comprises an O772P repeat sequence selected from the group consisting of any one of SEQ ID NOs: 512-540, 542-546 and 548-567;

Y comprises a sequence having at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 568;

n is an integer from 1 to 35;

wherein each X present in said polypeptide is different.

16. The polynucleotide of claim 15, wherein said polynucleotide comprises SEQ ID NO: 569.

17. The polynucleotide of claim 15, wherein n is from 15 to 25.

18. The polynucleotide of claim 15, wherein n is 20.

19. The polynucleotide of claim 15, wherein said polynucleotide is overexpressed in ovarian cancer cells compared with normal tissues.

20. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NOs: 464-477 and 512-569;

(b) complements of the sequences provided in SEQ ID NOs: 464-477 and 512-569;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NOs: 464-477 and 512-569;

(d) sequences that hybridize to a sequence provided in SEQ ID NOs: 464-477 and 512-569, under highly stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NOs: 464-477 and 512-569;

(f) sequences having at least 90% identity to a sequence of SEQ ID NOs: 464-477 and 512-569; and

(g) degenerate variants of a sequence provided in SEQ ID NOs: 464-477 and 512-569.

21. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences encoded by a polynucleotide of claim 20; and

(b) sequences having at least 80% identity to a sequence encoded by a polynucleotide of claim 20; and

(c) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 20.

22. An expression vector comprising a polynucleotide of claim 20 operably linked to an expression control sequence.

23. A host cell transformed or transfected with an expression vector according to claim 22.

24. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 21.

25. A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 21;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

26. A fusion protein comprising at least one polypeptide according to claim 21.

27. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) polypeptides according to claim 21;
- (b) polynucleotides according to claim 20; and
- (c) antigen-presenting cells that express a polynucleotide according to claim 20,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

28. An isolated T cell population, comprising T cells prepared according to the method of claim 27.

29. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 21;
- (b) polynucleotides according to claim 20;
- (c) antibodies according to claim 24;
- (d) fusion proteins according to claim 26;
- (e) T cell populations according to claim 28; and
- (f) antigen presenting cells that express a polypeptide according to claim 21.

30. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 29.

31. A method for the treatment of a ovarian cancer in a patient, comprising administering to the patient a composition of claim 29.

32. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide that hybridizes to a polynucleotide sequence according to claim 21 under moderately stringent conditions;
- (c) detecting in the sample an amount of said polynucleotide that hybridizes to the oligonucleotide; and
- (d) comparing the amount of said polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

33. An O772 polypeptide comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 490-511.

34. An O8E polypeptide comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 394-415.

35. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 1.

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11729.1 contg

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTGTTTTGTTTTGTTTTGTTTTG
TTTTGAGATGGAGTCTCACTCTGTTGCCAAGCTGGAGTACAACGGCATGATCTCAGCTCGCTGCAACCTCCGC
CTCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCAAGTAGCTGGGATTACAGGCGCCCGCCACCACGCTCA
GCTAATTTTTTTGTATTTTAGTAGAGACAGGGTTTACCAGGTTGGCCAGGCTGCTCTTGAACCTCCTGACCT
CAGGTGATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCCAAAG
CTGTTTCTTTGTCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGC
TCAGTCACTCCGTGGTC

11729-45.21.21.cons1

TAGGATGTGTTGGACCCTCTGTGTCAAAAAAACCTCACAAAGAATCCCCTGCTCATTACAGAAGAAGATGCAT
TAAAATATGGGTATTTTTCACTTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTCAGAAGAGATTGAA
TACCTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAATCAA
CTTTGATGACAGTAAAAATGGCCTTTCTGCATGGGAACCTATTGAGCTTATTGGAAATGGACAGTTAGCAAAG
GCATGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTTAATGAACCTATATTAGATGTGTTAAAGCAG
GGTTACATGATGAAAAAGGGCCACAGACGGAAAACTGGACTGAAAGATGGTTTGTACTAAACCCAACATAAT
TTCTTACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTTGGATGAAAATTGCTGTGTAGAGT
CCTTGCTGACAAAGATGGAAG

11729-45.21.21.cons2

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTGTTTTGTTTTGTTTTGTTTTG
TTTTGAGATGGAGTCTCACTCTGTTGCCAAGCTGGAGTACAACGGCATGATCTCAGCTCGCTGCAACCTCCGC
CTCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCAAGTAGCTGGGATTACAGGCGCCCGCCACCACGCTCA
GCTAATTTTTTTGTATTTTAGTAGAGACAGGGTTTACCAGGTTGGCCAGGCTGCTCTTGAACCTCCTGACCT
CAGGTGATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCCAAAG
CTGTTTCTTTGTCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGC
TCAGTCACTCCGTGGTC

11731.1contig

TCTTTTCTTTGATTTCTTCAATTTGTACGTTTGATTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTAT
TATAGCTTTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTT
TCAAGAGCATCTAATTGTTCTTTAAGTCTTTGGCATAATTCTTCTTTCTGATGACTTTTTATGAAGTAACT
GATCCCTGAATCAGGTGTGTTACTGAGCTGCATGTTTTAATTCTTTCGTTTAATAGCTGCTTCTCAGGGACCA
GATAGATAAGCTTATTTTGATATTCCTTAAGCTCTTGTGAAGTTGTTTGATTTCCATAATTTCCAGGTACAC
TGTTTATCCAAAATCTAGCTCAGTCTTTGTGTTTGCTTTCTGATTTGGACATCTTGTAGTCTGCCTGAGAT
CTGCTGATGXTTCCATTCACTGCTTCAGTTCAGGTGGAGACTTXXCTTTCTGGAGCTCAGCCTGACAATGC
CTTCTTGXTCCCT

Fig. 1A

2/101

11731.2contig

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGG
CCAAATATGTGGGCTATTACATCTGAAGAACGTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGG
AGGTTACATAACAGGTGATCAAGCCCGTACTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAA
TATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATC
AAGTTAAAGTTGCAGGGCCAACAGCTGCCTGTAGTCTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCC
ACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCAATCTGTCCATTCATCAGCCATTGCCTCCAGTTGCAC
CTATAGCAACACCTTGCTTCTGCTACTTCAGGGACCAGTATTCTCCCCTAATGATGCCTGCTCCCCTAGTG
CCTTCTGTAGTA

11734.1contig

AATAGATTTAATGCAGAGTGTCAACTTCAATTGATTGATAGTGGCTGCCTAGAGTGCTGTGTTGAGTAGGTTTC
TGAGGATGCACCCTGGCTTGAAGAGAAAGACTGGCAGGATTAACAATATCTAAATCTCACTTGTAGGAGAAAC
CACAGGCACCAGAGCTGCCACTGGTGTGGCACCAGCTCCACCAAGGCCAGCGAAGAGCCCAAATGTGAGAGTG
GCGGTGAGGTGGCACCAGCACTGAAGCCACCAGTGGTGTGGCACTGGCACTGGCACTGTTATTGGTACTGGT
ACTGGCACCAGTGTGGCACTGCCACTCTCTTGGGCTTTGGCTTTAGCTTCTGCTCCCGCTGGATCCGGGCTT
TGGCCAGGGTCCGATATCAGCTTCGTCCAGTTGCAGGGCCCGGCAGCATTCTCCGAGCCGAGCCCAATGCC
ATTCGAGCTCTAATCTCGGCCCTAGCCTTGGCTTCACTGCAGCCTCAGCTGCAGCCTTCAAATCCGCTTCCAT
CGCCTCTCGGTAC

11734.2contig

GCCAAGAAAGCCCGAAAGGTGAAGCATCTGGATGGGGAAGAGGATGGCAGCAGTGATCAGAGTCAGGCTTCTGG
AACCACAGGTGGCCGAAGGTCTCAAAGGCCCTAATGGCCTCAATGGCCCGCAGGGCTTCAAGGGTCCCATAG
CCTTTTGGGCGCAGGGCATCAAGGACTCGGTTGGCTGCTTGGGCGCGAGAGCCTTGCTCTCCCTGAGATCA
CCTAAAGCCCGTAGGGGCAAGGCTCGCCGTAGAGCTGCCAAGCTCCAGTCATCCCAAGAGCCTGAAGCACCACC
ACCTCGGGATGTGGCCCTTTGCAAGGGAGGGCAAATGATTTGGTGAAGTACCTTTTGGCTAAAGACCAGACGA
AGATTCCTCATCAAGCGCTCGGACATGCTGAAGGACATCATCAAAGAATACTGATGTGTACCCCGAAATCATT
GAACGAGCAGGCTATTCTTGGAGAAGGTATTTGGGATTCAATTGAAGGAAATTGATAAGAATGACCACTTGTA
CATTCTTCTCAGC

11736.1contg

GAGGTCTCACTATGTTGCCAGGCTGTTCTTGAACCTCTGGGATCAAGCAATCCACCCATGTTGGTCTCCAAAA
GTGCTGGGATCATAGGCGTGAGCCACCTCACCCAGCCACCAATTTTCAATCAGGAAGACTTTTTCTTCTTCAA
GAAGTGAAGGGTTTCCAGAGTATAGCTACACTATTGCTTGCTGAGGGTGACTACAAAATTGCTTGCTAAAAGG
TTAGGATGGGTAAAGAATTAGATTTTCTGAATGCAAAAATAAATGTGAACATAATGAACTTTAGGTAATACATA
TTCATAAAATAATTATTCACATATTTCTGATTTATCACAGAAATAATGTATGAAATGCTTTGAGTTTCTTGGGA
GTAACTCCATTACTCATCCCAAGAAACCATATTATAAGTATCACTGATAATAAGAACAACAGGACCTTGTCAT
AAATTCTGGATAAGAGAAATAGTCTCTGGGTGTTTGXTCTTAATTGATAAAATTTACTTGTCATCTTTTAGTT
CAGAATCACAAAA

Fig. 1B

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11736.2contig

AAGCGGAAATGAGAAAGGAGGGAAAATCATGTGGTATTGAGCGGAAAACCTGCTGGATGACAGGGCTCAGTCCTG
TTGGAGAACTCTGGGTGGTGCTGTAGAACAGGGCCACTCACAGTGGGGTGACAGACCAGCACGGCTCTGTGAC
CTGTTTGTACAGGTCCATGATGAGGTAAACAATACTGAGTATAAGGGTTGGTTTAGAACTCTTACAGCAA
TTTGACAAAGTAATCTTCTGTGCAGTGAATCTAAGAAAAAATTGGGGCTGTATTTGTATGTTCTTTTTTTCA
TTTCATGTTCTGAGTTACCTATTTTTATTGCATTTTACAAAAGCATCCTTCCATGAAGGACCGGAAGTTAAAA
CAAAGCAGGTCTTTATCACAGCACTGTCGTAGAACACAGTTCAGAGTTATCCACCCAAGGAGCCAGGGAGCTG
GGCTAAACCAAGAATTTTGCTTTTGGTTAATCATCAGGTACTTGAGTTGGAATTGTTTAAATCCCATCATTAC
CAGGCTGGAXGTG

11739-1&2

CCGCGGCTCCTGTCCAGACCCTGACCCTCCCTCCCAAGGCTCAACCGTCCCCAACCAACCGCCAGCCTTGACT
GATGTCGGCTGCGAGAGCCTGTGCTTAAGTAAGAATCAGGCCTTATTGGAGACATTCAAGCAAAGTTGGACAA
CTACTTTTCCAGAACAGAAAGGAACTCATGCATCAGAAAAGGTGACTAATAAAGGTACCAGAAGAATATGGCT
GCACAAATACCAGAATCTGATCAGATAAACAGTTTAAGGAATTTCTGGGGACCTACAATAAATTACAGAGAC
CTGCTTTTTGGACTGTGTTAGAGACTTCACAACAAGAGAAGTAAACCTGAAGAGACCACCTGTTCAGAACATT
GCTTACAGAAATATTTAAAAATGACACAAAGAATATCCATGAGATTTTCAGGAATATCATATTACAGCAGATGAA
GCCCTGGCAGCCAAAGCAGGACTCCTTGGCCAACCACGATAGAGAAGTCCTGATGGATGAACTTTGTGAAAG
ATTGCCAACAGCTGCTTTATTGGAAATGAGGACTCATCTGATAGAATCCCCTGAAAGCAGTAGCCACCATGTTT
AACCATCTGTCATGACTGTTTGGCAAATGGAACCGCTGGAGAAACAAAATTGCTATTTACCAGGAATAATCAC
AATAGAAGGTCTTATTGTTTCAGTGAAATAATAAGATGCAACATTTGTTGAGGCCTTATGATTACAGCAGCTTGGT
CACTTGATTAGAAAAATAAACCATGTTTCTTCAATTGTGACTGTTAATTTTAAAGCAACTTATGTGTTTCGATC
ATGATGAGATAGAAAAATTTTATTACTCAAAGTAAATAAATGGA

11740.1.contig

GAAAAAAATATAAACACACTTTTGCGAAAACGGTGGCCCTAAAAGAGGAAAAGAATTTACCAATATAAATC
CAATTTTATGAAAACCTGACAATTTAATCCAAGAATCACTTTTGTAAATGAAGCTAGCAAGTGATGATATGATAA
AATAAACGTGGAGGAAATAAAAAACAAGACTTGGCATAAGATATATCCACTTTTGATATTAACTTGTGAAGC
ATATTCTTCGACAAATTGTGAAAGCGTTCCTGATCTTGCTTGTCTCCATTTCAAATAAGGAGGCATATCACAT
CCCAAGAGTAACAGAAAAAGAAAAAGACATTTTGCATTTTGAGATGAACCAAGACACAAAACAAAACGAAC
AAAGTGTCTGTCTAATTCTAGCCTCTGAAATAAACCTTGAACATCTCTACAAGGCACCGTGATTTTTGTAAT
TCTAACCTGAAGAAATGTGATGACTTTTGTGGACATGAAAATCAGATGAGAAAACCTGTGGTCTTTCCAAAGCCT
GAACCTCCCTGAAAACCTTTGCA

Fig. 1C

4/101

11766.1.contig

CTGGGATCATTTCTCTTGATGTCATAAAAGACTCTTCTTCTCCTCTTCATCCTCTTCTTCATCCTCTTCTGTGTA
CAGTGCTGCCGGGTACAACGGCTATCTTTGTCTTTATCCTGAGATGAAGATGATGCTTCTGTTTCTCCTACCAT
AACTGAAGAAATTTGCTGGAAGTCGTTTGACTGGCTGTTTCTGACTTCACCTTCTTTGTCAAACCTGAGTC
TTTTTACCTCATGCCCTCAGCTTCCACAGCATCTTCATCTGGATGTTTATTTTTCAAAGGGCTCACTGAGGAA
ACTTCTGATTGAGAGTCGAAGAGTCACTGTGATTTTTCTCCTCATTTTGCTGCAAATTTGCCTCTTTGCTGTC
TGTGCTCTCAGGCAACCCATTTGTTGTCATGGGGGCTGACAAAGAAACCTTTGGTCGATTAAGTGGCCTGGGTG
TCCAGGCCCATTTATATTAGACCTCTCAGTATAGCTTGGTGAATTTCCAGGAAACATAACACCATTCAATCGA
TTTAAACTATTGGAATTGGTTTT

11766.2.contig

GAGGGTTGGTGGTAGCGGCTTGGGGAGGTGCTCGCTCTGTGGTCTTGCTCTCTCGCACGCTTCCCCGGCTCC
CTTCGTTTCCCCCCCCGGTCGCCTGCGTGCCGGAGTGTGTGCGAGGGAGGGGAGGGCGTCGGGGGGGTGGGG
GGAGGCGTTCGGTCCCCAAGAGACCCGCGGAGGGAGGCGGAGGCTGTGAGGGACTCCGGGAAGCCATGGACGT
CGAGAGGCTCCAGGAGGCGCTGAAAGATTTTGAGAAGAGGGGGAAAAAGGAAGTTTGTCTGTCTGGATCAGT
TTCTTTGTATGTAGCCAAGACTGGAGAAACAATGATTAGTGGTCCCAATTTAAAGGCTATTTTATTTTCAA
CTGGAGAAAGTGATGGATGATTTCAGAACTTCAGCTCCTGAGCCAAGAGGTCTCCCAACCCTAATGTGCA

11773.2.contig

AAGCAGGCGGCTCCCGCGCTCGCAGGGCCGTGCCACCTGCCCGCCCGCCGCTCGCTCGCTCGCCGCGCGGCC
GCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGCTGCCCCGCGCTGCCGXTGCCG

11775-1&2

ATCTCTTGATGCCAAATATTTAATATAAATCTTTGAAACAAGTTCAGATGAAATAAAATCAAAGTTTGCAAA
AACGTGAAGATTAACCTAATTGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTTATTTCTATGCAAAA
GTATGCCTTCAAAGTCTTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCATC
TTGCAATTGTAAGAAATAGGTAAAAGATTATAAGACACCTTACACACACACACACACACACAGTGTGCACG
CCAATGACAAAAACAATTTGGCCTCTCTAAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGGGAACA
CTGTGTCACCCCTCCCTACAATCCAGGTAGTTTCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGT
GATTCTGACAGCCACGTTGAAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGCCCTGAAAAATGCCAA
TAATTTTTCGCTCCCACTTCTGCTGCTGtCTCTCCACATCCTCACATAGACCCAGACCCGCTGGCCCCCTGGC
TGGGCATCGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTCACAGAAGCGATACACCAAATTGCC
TGGTCGGTCATTGTCATAACCAGAGA

Fig. 1D

5/101

11777.1&2.cons

CAGACGGGGTTTCACTATGTTGGCTAGGCTGGTCTTGAACCTCTGACTTCAGGTGATCTGCCTGCCTTGGCCTC
CCAAAGTGCTGGGATTACAGGCATAAGCCACTGCGCCCGGCTGATCTGATGGTTTCATAAGGCTTTTCCCCCTT
TTGCTCAGCACTTCTCCTTCTGCGCCATGTGAAGAAGGACATGTTTGCTTCCCCTTCCACCAGATTGTAAG
TTGTTTCTGAGGCCTCCCCGGCCATGCTGAACGTGTGAGTCAATTAACCTCTTTCTTTATAAATTATCCAGT
TTTGGGTATGTCTTTATTAGTAGAATGAGAACAGACTAATAACAACCTTAAAGGAGACTGACGGAGAGGATTCT
TCCTGGATCCCAGCACTTCTCTGAATGCTACTGACATTCTTCTTGAGGACTTTAACTGGGAGATAGAAAACA
GATTCCATGGCTCAGCAGCCTGAGAGCAGGGAGGGAGCCAAGCTATAGATGACATGGGCAGCCTCCCCTGAGGC
CAGGTGTGGCGGAACCTGGGCAGTGTGCACCCACCCACCAGGGCCAAGTCTGTCTTGGAGAGCCAAGCC
TCAATCACTGCTAGCCTCAAGTGTCCCAAGCCACAGTGGCTAGGGGGACTCAGGGAACAGTTCCAGTCTGCC
CTACTTCTCTTACCTTTACCCCTCATACCTCCAAAGTAGACCATGTTTATGAGGTCCAAAGG

11779.2.contig

AAGCGAGGAAGCCACTGCGGCTCCTGGCTGAAAAGCGGCGCCAGGCTCGGGAACAGAGGGAACGCGAAGAACAG
GAGCGGAAGCTGCAGGCTGAAAGGGACAAGCGAATGCGAGAGGAGCAGCTGGCCCGGGAGGCTGAAGCCCGGGC
TGAACGTGAGGCGAGGCGCGGAGACGGGAGGAGCAGGAGGCTCGAGAGAAGGCGCAGGCTGAGCAGGAGGAGC
AGGAGCGACTGCAGAAGCAGAAAGAGGAAGCCGAAGCCCGGTCCCGGAAGAAGCTGAGCGCCAGCGCCAGGAG
CGGGAAAAGCACTTTTCAAGAGGAGAACAGGAGAGACAAGAGCGAAGAAAGCGGCTGGAGGAGATAATGAAGAG
GACTCGGAAATCAGAAGCCGCCGAAACCAAGAAGCAGGATGCAAAGGAGACCGCAGCTAACAATTCGGGCCAG
ACCTTGTGAAAGCTGTAGAGACTCGGCCCTCTGGGCTTCAGAAAGGATTCTATTGCAGAAAGGAAGGAGCTX
GGCCCCCAXGGA

11781 & 37.cons

CTCTGTGGAAAAGTCTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGA
TTACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGA
TTCATACTACCCACACAGACCGGTTTCTCTCAGTGTGACCTACACACTCACTGCTCTTACCAGATGATG
TTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCCAAGTTCCAGGAACTGGATTCTTTAACTAACTGACCATGG
ACTAGAGGAGATTTCTTCTGTGCGCCAGAAAGGATTTATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCT
GCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTC
CAAGAACAACAAAACCATATCAGTGTACTGTAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTG
TAGATAGTAGAAAGGGGGCATCACXTGAGAAAGAGCTGATTTTGTATTTAGGTTTGAAAAGAAATAACTGAA
CATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACCTCAGAAATTAAGTTACTCA
GAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCATATACCCTTCTTCTGGATTACCA
ATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTAATTTCAATTTGTTTATATTTACCTCTG
GGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTAGAAAATCTTTTGGATTTTCTGTGGTTTATGG
CAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACATC
CCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTTCAAGATATTTTCTCTACAATAAAGTA
ACAAT

Fig. 1E

6/101

11781-76-87-37

CTCTGTGGAAAAGTATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGA
TTACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGA
TTCATACTCACCCACACAGACCGGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCAGATGATG
TTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCAGGAAACTGGATTCTTTAACTAACTGACCATGG
ACTAGAGGAGATTTCTTCTGTGCGCAGAAAGGATTTATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCT
GCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTC
CAAGAACAACAAAACCATATCAGTGTACTGTAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTG
TAGATAGTAGAAAGGGGGGCATCACCTGAGAAAGAGCTGATTTTGTATTTAGGTTTGAAAAGAAATAACTGAA
CATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAAGTCAAGAAATTAAGTTACTCA
GAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCATATACCTTCTTCTGGATTACCA
ATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTAATTTCAATTTGTTTATTTACCTCTG
GGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTGGATTTTCTGTGGTTTATGG
CAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACATC
CCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTAGGATATTTTCTCTACAATAAAGTA
ACAATTA

11784-1 & 2

GGACGACAAGGCCATGGCGATATCGGATCCGAATTCAGCCTTTGGAATTAATAAACCCTGGAACAGGGAAGGT
GAAAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGTGCACAGTTGAATGGGAAGTGTGGGTTTAGGGC
ATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTGGGAGGTCAAGTGGGGAAGTTGGTGAATGTGGA
ATAACTTACCTTTGTGCTCCACTTAACCAGATGTGTTGCAGCTTTCTGACATGCAAGGATCTACTTTAATTC
CACACTCTCATTATAAATTGAATAAAAGGGAATGTTTTGGCACCTGATATAATCTGCCAGGCTATGTGACAGT
AGGAAGGAATGGTTTCCCCTAACAAGCCCAATGCACTGGTCTGACTTTATAAATTATTTAATAAATGAAGTAT
TATC

11785.2.contig

GGCAGTGACATTCACCATCATGGGAACCACTTCCCTTTTCTTCAAGATTCTCTGTAGTGGAAGAGAGACCCCA
GTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGTGC
CAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTGGAATCGCCAAGTCAAACTTTCTAACT
TCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAAGTGGTGTTACC
CAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAACAGGATGTGCTTTCCTTTGCC
ATTTAGGGTTTCTTCTTTCTTTCTTTCTTTATTAACCACT

Fig. 1F

7/101

11718-1&2 cons

TGCGCTGAAAACAACGGCCTCCTTTACTGTTAAATGCAGCCACAGGTGCTTAGCCGTGGGCATCTCAACCACC
AGCCTCTGTGGGGGGCAGGTGGGCGTCCCTGTGGGCCTCTGGGCCCACGTCCAGCCTCTGTCTCTGCCTTCCG
TTCTTCGACAGTGTTCCCGGCATCCCTGGTCACTTGGTACTTGGCGTGGGCCTCCTGTGCTGCTCCAGCAGCTC
CTCCAGGXGGTCGGCCCGCTTACCGCAGCCTCATGTTGTGTCCGAGGCTGCTCACGGCCTCCTCCTTCCTCG
CGAGGGCTGTCTTACCCTCCGXGCACCTCCTCCAGTCCAGCTGCTGGCGGGCCTGCAGCGTGGCCAGCTCG
GCCTTGGCCTGCCGCGTCTCCTCCTCARAGGCTGCCAGCCGGTCTCGAACTCCTGGCGGATCACCTGGGCCAG
GTTGCTGCGCTCGCTAGAAAGCTGCTCGTTCACCGCTGCGCATCCTCCAGCGCCCGCTCCTTCTGCCGCACAA
GGCCCTGCAGACGAGATTCTCGCCCTCGGCCTCCCAAGCTGGCCCTTCACTCCGAGCACCCTCCTGAAGC
TTCGCTCCGACTGCTCCAGCTCGGAGAGCTCGGCCTCGTACTTGTCCCGTAAGCGCTTGATGCGGCTCTCGGC
AGCCTTCTCACTCTCCTCCTTGGCCAGCGCCATGTCGGCTCCAGCCGGTGAATGACCAGCTCAATCTCCTTGT
CCCGGCCTTTCGGATTCTTCCCTCAGCTCCTGTTCCCGGTTCAAGCAGCCACGCTCCTCCTTCTGGTGCGG
CCGGCCTCCACGCTGCCTCTCCAGCTCCAGCTGCTGCTTCAAGGTATTAGCTCCATCTGGCGGGCCTGCAG
CGTGGCCA

13690.4

CAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTTCCAGGCTGTGATATATTTTCTAGTGGT
TTGACTTTAAAAATAAATAAGGTTAATTTTCTCCCC

13693.1

TGCAAGTCACGGGAGTTTATTTATTTAATTTTTTTTCCCCAGATGGAGACTCTGTGCGCCAGGCTGGAGTGCAAT
GGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCTGCCACAGCCTCCCGAGTAGC
TGGGATTACAGGTGCCCGCCACCACCCAGCTAATTTTTATATTTTATAGTAAAGACAGGGTTTCCCATGTTG
GCCAGGCTGGTCTTGAACCTTCTGACCTCAGGTGATCCACCTGCCTCGGCCTCCCAAAGTGTTGGGATTACAGGC
GTGAGCTACCCGTGCCTGGCCAGCCACTGGAGTTTAAAGGACAGTCATGTTGGCTCCAGCCTAAGGCGGCATTT
TCCCCATCAGAAAGCCCGCGGCTCCTGTACCTCAAAATAGGGCACCTGTAAAGTCAGTCAGTGAAGTCTCTGC
TCTAACTGGCCACCCGGGGCCATTGGCCTCTGACACAGCCTTGCCAGGANGCCTGCATCTGCAAAAGAAAAGTT
CACTTCCTTTCCG

13694.1

CAGAGAATCTKAGAAAGATGTGCGTTTTCTTTTAAATGAATGAGAGAAGCCATTTGTATCCCTGAATCATTGA
GAAAAGGCGGCGGTGGCGACAGCGGCGACCTAGGGATCGATCTGGAGGGACTTGGGGAGCGTGACAGACCTCT
AGCTCGAGCGGAGGGACCTCCGCGGGGATGCCTGGGAGCAGATGGACCCTACTGGAAGTCAGTTGGATTCA
GATTTCTCTCAGCAAGATACTCCTTGCTGATAATTGAAGATTCTCAGCCTGAAAGCCAGGTTCTAGAGGATGA
TTCTGGTTCTCACTTCACTATGCTATCTCGACACCTTCTAATCTCCAGACGCACAAAGAAAATCCTGTGTTGG
ATGTTGNGTCCAATCCTTGAAACAAACAGCTGGAGAAGAACGAGGAGACCGGTAATAGTGGGTTCAATGAACATT
TGAAAGAAAACAGGTTGCAGACCCTG

Fig. 1G

8/101

13694.2

GACTGTCCTGAACAAGGGACCTCTGACCAGAGAGCTGCAGGAGATGCAGAGTGGTGGCAGGAGTGGAAGCCAAA
GAACACCCACCTTCCTCCCTTGAAGGAGTAGAGCAACCATCAGAAGATACTGTTTTATTGCTCTGGTCAAACAA
GTCTTCCTGAGTTGACAAAACCTCAGGCTCTGGTGACTTCTGAATCTGCAGTCCACTTTCCATAAGTTCTTG
CAGACAACTGTTCTTTTGCTTCCATAGCAGCAACAGATGCTTTGGGGCTAAAAGGCATGTCCTCTGACCTTGCA
GGTGGTGGATTTTGCTCTTTTACAACATGTACATCCTTACTGGGCTGTGCTGTCACAGGGATGTCCTTGCTGGA
CTGTTCTGCTATGGGGATATCTTCGTTGGACTGTTCTTCATGCTTAATTGCAGTATTAGCATCCACATCAGACA
GCCTGGTATAACCAGAGTTGGTGGTACTGATTGTAGCTGCTCTTGTCCACTTCATATGGCACAAGTATTTTC
CTCAACATCCTGGCTCTGGGAAG

13695.1

GAAATGTATATTTAATCATTCTCTTGAACGATCAGAACTCTRAAATCAGTTTTCTATAACARCATGTAATACAG
TCACCGTGGCTCCAAGGTCCAGGAAGGCAGTGGTTAACACATGAAGAGTGTGGGAAGGGGGCTGGAAACAAAGT
ATTCTTTTCTTCAAAGCTTCATTCTCAAGGCCTCAATTCAAGCAGTCATTGTCCTTGCTTTCAAAGTCTGT
GTGTGCTTCATGGAAGGTATATGTTTGTGCTTAATTTGAATTGTGGCCAGGAAGGGTCTGGAGATCTAAATT
CAGAGTAAGAAAACCTGAGCTAGAACTCAGGCATTTCTTACAGAACTTGGCTTGCAAGGTAGAATGAANGGA
AAGAACTTAGAAGCTCAACAAGCTGAAGATAATCCCATCAGGCATTTCCATAGGCCTTGCAACTCTGTTTAC
TGAGAGATGTTATCCTG

13695.2

AGTCTGGAGTGAGCAAAACAAGAGCAAGAAAACAARRAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAA
ATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGAGTGATAA
GTAAAATGCACGTGGAGACAAGTGCATCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCTGGGGAGTGAGA
GGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTGTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCC
TGGAAGTCTATCCCAACATATCCACATCTTATATTCCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGC
TAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTGTATATGGGTCAAATGATTCACTTTTTATGATG
CTTCCAAGGTGCCTTGGCTTCTCTTCCCACTGACAAATGCCCAAGTTGAGAAAAATGATCATAATTTTAGCA
TAAACCGAGCAATCGGCGACCCC

13697.1

TAGCTGTCTTCCTCACTCTTATGGCAATGACCCCATATCTTAATGGATTAAGATAATGAAAGTGTATTTCTTAC
ACTCTGTATCTATCACCAGAAGCTGAGGTGATAGCCCGCTTGTCTTGTGTCATCCATATTCTGGGACTCAGGCGG
GAACTTTCTGGAATATTGCCAGGGAGCATGGCAGAGGGGCACAGTGCATTCTGGGGGAATGCACATTGGCTCAG
CCTGGGTAATGAGTGATATACATTACCTCTGTTCAAACTCATTGCCAGCACCAGTCACAAGGCCCCACCAAA
TACCAGAGCCCAAGAAATGTAGTCTGTGATATGGTTTTGCTGTGTCCCAACCCAAATCTCATCTTGAATTGT
AAGCTCCCATAAATCCCATGTGTTGTGGGAGGGACCTGGTG

Fig. 1H

9/101

13697.2

ATCATGAGGATGTTACCAAAGGGATGGTACTAAACCATTTGTATTGCTCTGTTTTCACACTGCTTTGAAGATAC
TACCTGAGACTGGGTAATTTATAAACAAAAGAGATTTAATTGACTCACAGTTCTGCATGGCTGAAGAGGCCTCA
GGAACTTACAGTCATGGTGGGAAGGCAAAGGAGGAGCAAGGCATGTCTTACATGTCAGTAGGAGAGAGAGCGAG
AGCAGGAGAACCTGCCACTTATAAACCATTCAGATCTCATAACTCCCTATCATGAGAAAAACATGGAGGAAACC
ACCCTCATGATCCAATCACCTCCCGCCAGGTCCCTCCCTCGACACGTGGGGATTATAATTGAGGATTAGAGGGA
CACAGAGACAAACCATATCATCATTGAGAGAAATCCACCCTCATAGTCCAATCAGCTCCTACCAGGCCCCACC
TCCAACACTGGGGATTGCAATTCAACATGAGATTTGGATGGGGACACAGATTCAAACCATATCATAC

13699.1&2

CATGGCCTTTCTCCTTAGAGGCCAGAGGTGCTGCCCTGGCTGGGAGTGAAGCTCCAGGCACTACCAGCTTTCTT
GATTTTCCCGTTTGGTCCATGTGAAGAGCTACCACGAGCCCCAGCCTCACAGTGCTCACTCAAGGGCAGCTTGG
TCCTCTTGTCTGCAGAGGCAGGCTGGTGTGACCCTGGGAACCTGACCCGGGAACAACAGGTGGCCCAGAGTGA
GTGTGGCCTGGCCCCCTAACCTAGTGTCCGTCTCTCTCTCTGGAGCCAGTCTTGAGTTTAAAGGCATTAAG
TGTTAGATACAAGCTCCTTGTGGCTGGAAAAACACCCCTCTGCTGATAAAGCTCAGGGGGCACTGAGGAAGCAG
AGGCCCCCTGGGGGTGCCCTCCTGAAGAGAGCGTCAGGCCATCAGCTCTGTCCCTCTGGTGTCCACGTCTGT
TCCTCACCTCCATCTCTGGGAGCAGCTGCACCTGACTGGCCACGCGGGGGCAGTGGAGGCACAGGCTCAGGGT
GGCCGGGCTACCTGGCACCTATGGCTTACAAAGTAGAGTTGGCCAGTTTCTTCCACCTGAGGGGAGCACTC
TGACTCCTAACAGTCTTCTTGGCTGCCATCATCTGGGTGGCTGGCTGTCAAGAAAGGCCGGGCATGCTTTC
TAAACACAGCCACAGGAGGCTTGTAGGCATCTTCCAGGTGGGGAAACAGTCTTAGATAAGTAAGGTGACTTGC
CTAAGGCCTCCAGCACCTTGATCTTGGAGTCTCACAGCAGACTGCATGTSAAACACTGGAACCGAAAAACATG
CCTCAGTATAAAA

13703.3

CCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCTCTTGGAGACACAGAGGGTTTCACCTTGGATGACCTCTA
GAGAAATTGCCAAGAAGCCACCTTCTGGTCCCAACCTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGC
TGTAAGGTCACTTGGCTCCATTGCCTGCTTCCAACCAATGGGCAGGAGAGAAGGCCTTTATTTCTGCCCCAC
CCATTCTCCTGTACCAGCACCTCCGTTTTGAGTCAGYGTGTCCAGCAACGGTACCGTTTACACAGTCA

13705.1

TGCATGTAGTTTTATTTATGTGTTTTSGTCTGGAAAACCAAGTGTCAGCAGCATGACTGAACATCACTCACT
TCCCCTACTTGATCTACAAGGCCAACGCCGAGAGCCCAGACCAGGATTCCAACACACTGCACGAGAATATTGT
GGATCCGCTGTGAGGTAAGTGTCCGTCACTGACCCARACGCTGTTACGTGGCACATGACTGTACAGTGCCACGT
AACAGCACTGTACTTTTCTCCATGAACAGTTACCTGCCATGTATCTACATGATTCAGAACATTTTGAACAGTT
AATTCTGACACTTGAATAATCCCATCAAAAACCGTAAATCACTTTGATGTTTGTAAACGACAACATAGCATCAC
TTTACGACAGAATCATCTGAAAAACAGAAACGAATACATACATCTTAAAAATGCTGGGGTGGGCCAGGCA
CAGCTTACGCCTGTAATCCAGCACTTTGGGAGGCTTAAGCGGGTG

Fig. 11

10/101

13705.2

TGGGGCGGAAAGAAGCCAAGGCCAAGGAGCTGGTGC GGCAGCTGCAGCTGGAGGCCGAGGAGCAGAGGAAGCAG
AAGAAGCGGCAGAGTGTGTGGGCCTGCACAGATACCTTCACTTGCTGGATGGAAATGAAAATTACCCGTGTCT
TGTGGATGCAGACGGTGATGTGATTTCTTCCCACCAATAACCAACAGTGAGAAGACAAAGGTTAAGAAAACGA
CTTCTGATTTGTTTTTGAAGTAACAAGTGCCACCAGTCTGCAGATTTGCAAGGATGTCATGGATGCCCTCATT
CTGAAAATGGCAAGAAATGAAAAAGTACACTTTAGAAAATAAAGAGGAAGGATCACTCTCAGATACTGAAGCCG
ATGCAGTCTCTGGACAACCTCCAGATCCCACAACGAATCCAGTGCTGGAAAGGACGGGCCCTTCTTCTGGTG
GTGGAACANGTCCCGGTGGTGGATCTTGGAANGAACCTGAANGTGGTGTACCCCGTCCAAGGCCGACCTTGGC
CAC

13707.4

TCCCGCGCTCGCAGGGCNCGTGCCACCTGCCYGTCCGCCGCTCGCTCGCTCGCCGCCGCGCCGCGCTGCCGA
CCGYCAGCATGCTGCCGAGAGTGGGCTGCCCCGCGTGCCGCTGCCGCCGCCGCGCTGCTGCCGCTGCTGCCG
CTGCTGCTGCTGC

13708.1&2

GGCGGGTAGGCATGGAAGTGAAGAAGCAAGAAGCTTTCACTACGTGGGGAAGAATGAAAAACCAAAT
ATGCCAAGATTCAGCAAAGGGGACAGGGAGCTCCAGCCGAGAGCCTATTATTAGCAGTGAGGAGCAGAAGCA
GCTGATGCTGTACTATCACAGAAGACAAGAGGAGCTCAAGAGATTGGAAGAAATGATGATGATGCCTATTTAA
ACTCACCATGGGCGGATAAACTGCTTTGAAAAGACATTTTCATGGAGTGAAAGACATAAAGTGGAGACCAAGA
TGAAGTTCACCAGCTGATGACACTTCCAAAGAGATTAGCTCACCT

13709.1

TCTGAAGGTTAAATGTTTCATCTAAATAGGGATAATGRTAAACACCTATAGCATAGAGTTGTTTGAGATTAAAT
GAGATAATACATGTAAAATTATGTGCCTGGCATAACAGCAAGATTGTTGTTGTTGTTGATGATGATGATGATGAT
GATAATATTTTTCTATCCCCAGTGCAAACTGCTTGAACCTATTAGATAATCAATACATGTTTCTTGAAGTGA
ATCAATTTCCCATGTTGTCTGACTGATGAAGCCCTACATTTTCTTCTAGAGGAGATGACATTTGAGCAAGATC
TTAAAGAAAATCAGATGCCTTCACCTGACCACTGCTTGGTGATCCCATGGCACTTTGTACATCTCTCCATTAGC
TCTCATCTCACCAGCCCATATTATTGTATGTGCTGCTTCTGAAGCTTGCAGCTGGCTACCATCMGGTAGAAT
AAAAATCATCCTTTCATAAAATAGTGACCCTCCTTTTTTATTTGCATTTCCCAAAGCCAAGCACCGTGGGANGG
TAG

Fig. 1J

11/101

13709.2

TATGAAGAAGGGAAAAGAAGATAATTTGTGAAAGAAATGGGTCCAGTTACTAGTCTTTGAAAAGGGTCAGTCTG
TAGCTCTTCTTAATGAGAATAGGCAGCTTTCAGTTGCTCAGGGTCAGATTTCTTAGTGGTGTATCTAATCACA
GGAAACATCTGTGGTTCCTCCAGTCTCTTCTGGGGGACTTGGGCCACTTCTCATTTCATTTAATTAGAGGA
AATAGAACTCAAAGTACAATTTACTGTTGTTTAAACAATGCCACAAAGACATGGTTGGGAGCTATTTCTTGATTT
GTGTAAAATGCTGTTTTTGTGTGCTCATAATGGTTCCAAAAATTGGGTGCTGGCCAAAGAGAGATACTGTTACA
GAAGCCAGCAAGAAGACCTCTGTTTCATTACACCCCCGGGGATATCAGGAATTGACTCCAGTGTGTGCAAATCC
AGTTTGGCCTATCTTCT

13712.1&2

TGAGGGACTGATTGGTTTGCTCTCTGCTATTCAATTCCTCAAGCCACTTGTTCTGCAGCGTCCTCCTTCTCA
TTCCCTTTAGTTGTACCCTCTCTTTCATCTGAGACCTTTCCTTCTTGATGTCGCCCTTTTCTTCTTGCTTTT
TCTGATGTTCTGCTCAGCATGTTCTGGGTGCTTCTCATCTGCATCATTCTTTCAGATGCTGTAGCTTCTTCT
CCTCTTTCTGCCCTCCTTTTCTTTTCTTTTTTTGGGGGGCTTGCTCTCTGACTGCAGTTGAGGGGCCCCAGGG
TCCTGGCCTTTGAGACGAGCCAGGAAGGCCTGCTCCTGGGCCTCTAGGCGAGCAAGCTTGGCCTTCATTGTGAT
CCCAAGACGGGCAGCCTTGTGTGCTGTTGCCCCCTCACAGGCTTGGAGCAGCATCTCATCAGTCAGAATCTTTG
GGGACTTGGACCCCTGGTTGTGTCATCACTGCAGCTCTCCAAGTCTTTGTTTGGCTTCTCTCCACCTGAAGTC
AATGTAGCCATCTTCACAACTTCTGATACAGCAAGTTGGGCTTGGGATGATTATAACGGGTGGTCTCCTTAGA
AAGGCTCCTTATCTGTACTCCATCCTGCCAGTTTCCACTACCAAGTTGGCCGAGTCTTGTGAAGAGCTCAT
TCCACCAGTGGTTTGTGAACCTCTTGGCAGGGTCATGTCCTACCCCATGAGTGTCTTGCTTCAGYGTACCCCTG
AGAGCCTGAGTGATACCATTCTCCTCCG

13714.1&2

GACAACATGAAATAAATCCTAGAGGACAAAATTAACCTCAATAGAGTGTAGTCTAGTTAAAACTCGAAAAATG
AGCAAGTCTGGTGGGAGTGGAGGAAGGGCTATACTATAAATCCAAGTGGGCCTCCTGATCTTAACAAGCCATGC
TCATTATACACATCTCTGAACTGGACATACCACCTTACGCAGGAAACAGGGCTTGAACCTCTAAGGGAAATT
AACATGCACCACCCACATCTAACCTACCTGCCGGGTAGGTACCATCCCTGCTTCGCTGAAATCAGTGCTC

13716.1&2

TTGGAATTAAATAAACCTGGAACAGGGAAGGTGAAAGTTGGAGTGAGATGTCTTCATATCTATACCTTTGTGC
ACAGTTGAATGGGAAGTGTGTTGGTTTAGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGT
GGAGGTCAAGTGGGGAAGTTGGTGAATGTGGAATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAG
CTTTCCTGACATGCAAGGATCTACTTTAATTCCACACTCTCATTAATAAATTGAATAAAAGGGAATGTTTTGGC
ACCTGATATAATCTGCCAGGCTATGTGACAGTAGGAAGGAATGGTTTCCCTAACAAAGCCCAATGCACTGGTCT
GACTTTATAAATTATTTAATAAAATGAACATTATC

Fig. 1K

12/101

13718.2

AAACTGGACCTGCAACAGGGACATGAATTTACTGCARGGTCTGAGCAAGCTCAGCCCCTCTACCTCAGGGCCCC
ACAGCCATGACTACCTCCCCAGGAGCGGGAGGGTGAAGGGGGCCTGTCTCTGCAAGTGGAGCCAGAGTGGAGG
AATGAGCTCTGAAGACACAGCAGCCAGCCTTCTCGCACCAGCCAAGCCTTAAGTGCCTGCCTGACCCCTGAACCA
GAACCCAGCTGAACTGCCCCCTCAAGGGACAGGAAGGCTGGGGGAGGGAGTTACAACCCAAGCCATTCACCC
CCTCCCCTGCTGGGGAGAATGACACATCAAGCTGCTAACAAATTGGGGGAAGGGGAAGGAAGAACTCTGAAAA
CAAAATCTTGT

13722.3

CATGCGTTTCACCACTGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGCAATCCACCCGCCTCAGCCTCCA
AAAGTGCCTGGGATTACAGATGTGAGCCATGGCACCATGCCAAAAGGCTATATTCCTGGCTCTGTGTTCCGAGA
CTGCTTTTAAATCCCAACTTCTCTACATTTAGATTAAAAAATATTTTATTCATGGTCAATCTGGAACATAATTAC
TGCATCTTAAGTTTCCACTGATGTATATAGAAGGCTAAAGGCACAATTTTTATCAAATCTAGTAGAGTAACCAA
ACATAAAATCATTAATTACTTTCAACTTAATACTAATTGACATTCCTCAAAGAGCTGTTTTCAATCCTGATA
GGTTCTTTATTTTTTCAAATATATTTGCCATGGGATGCTAATTTGCAATAAGGCGCATAATGAGAATACCCCA
AACTGGA

13722.4

GTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCCGAGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTA
TGCTTCTGGATCCGAATTTGATGAGATGTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAG
CAAAGGCGAATGCTCCTTGTTATATTTATTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCA
ATGCATCCATATTCAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCAATGAAGGAGT
TATCATAATAGGAGCCACAACTTCCCAGAGGCATTAGATAATGCCTTAATACCGTCTGGTCGTTTTGACATG
CAAGTTACAGTTCCAAGGCCAGATGTAAAAGGTCGAACAGAAATTTTGAATGGTATCTCAATAAAATAAAGTT
TGATCAATCCCGTTGATCCAGAAATTATAGCCTCGAGGTACTGGTGGCTTTTCCGGAAGCAGAGTTGGGAGAAT
CTT

13724-13698-13748

GCCTACAACATCCAGAAAGAGTCTACCCTGCACCTGGTGTCTCGTCTCAGAGGTGGGATGCAGATCTTCGTGAA
GACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCGAGTGACACCATYGAGAACGTCAAAGCAAAGATCC
ARGACAAGGAAGGCRTYCCTCCTGACCAGCAGAGGTTGATCTTTGCCGAAAGCAGCTGGAAGATGGDCGCACC
CTGTCTGACTACAACATCCAGAAAGAGTCYACCCTGCACCTGGTGTCTCCGTCTCAGAGGTGGGATGCARATCTT
CGTGAAGACCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCCAGTGACACCATCGAGAATGTCAAGGCAA
AGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGA
CGCACCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACCTGGTCTGCGCTTGAGGGGGGTGTCTA
AGTTTCCCCTTTAAGGTTTTCMAAAATTTTCATTGCACTTTCCTTTCAATAAAGTTGTTGCATTCCC

Fig. 1L

13/101

13730.1

GAAGTGGGCCCTGAGCCCAAGTCATGCCTTGTGTCCGCATCTGCCGTGTCACCTCTGTCCTGCCCTCACCCC
TCCCTCCTGGTCTTCTGAGCCAGCACCATCTCCAAATAGCCTATTCTTCCTGCAAATCACACACATGCGGG
CCACACATACCTGCTGCCCTGGAGATGGGGAAGTAGGAGAGATGAATAGAGGCCCATACATTGTACAGAAGGAG
GGGCAGGTGCAGATAAAAGCAGCAGACCCAGCGGCAGCTGAGGTGCATGGAGCACGGTTGGGGCCGGCATTGGG
CTGAGCACCTGATGGGCCTCATCTCGTGAATCTCGAGGCAGCGCCACAGCAGAGGAGTTAAGTGGCACCTGGG
CCGAGCAGAGCAGGAGACTGAGGGTCAGAGTGGAGGCTAAGCTGCCCTGGAACCTCTCAATCTTGCTGCCCCC
TAGTATGAAGCCCCCTTCTGCCCTACAATTCCTGA

13732.1

ATGGATCTTACTTTGCCACCCAGGTTGGAGTGCAGTGTGCAATCTTGGCTCACTGCAGCCTTAACCTCCCAGG
CTCAAGCTATCCTCCTGCCAAAGCCTTCCACATAGCTGGGACTACAGGTACACNGCCACCACCCAGCTAAAA
TTTTTGTATTTTTGTAGAGACGGGATCTCGCCACGTTGCCAGGCTGGTCCCATCCTGACCTCAAGCAGATCT
GCCACCTCAGCCCCCAACGTGCTAGGATTACAGGCGTGAGCCACCGCACCCAGCCTTTGTTTTGCTTTTAAT
GGAATCACCAGTTCCCCTCCGTGTCTCAGCAGCAGCTGTGAGAAATGCTTTGCATCTGTGACCTTTATGAAGGG
GAATTCATGCTGAATGAGGGTAGGATTACATGCTCCTGTTTCCCGGGGTCAAGAAAGCCTCAGACTCCAGC
ATGATAAGCAGGGTGAG

13732.2

ATAGGGGCTTTAAGGAGGGAATTCAGGTTCAATGAGGTCGTAAGGCCAGGGCTCTTATCCAGTAAGACTGGGGT
CCTTAGATGAGAAAGAGACACCCGAGGTCCTTCTCTGCCGTGTGAGGATGCATCAAGAAGGCGGCCGTCTGC
AAGCGAAGGAGAGGCCGACCCAGAAACCGACACCTTCATCTTGGACTTGACGCTCTAGAACTGAGAAAAATAAC
TGTCTGTTGGTTAAGCCACCCAGTTTGTAGTATTCTTATGGCTTCCTAAGCAGACTAACAACAAACACCCA
AAATTAAGTATGGCTTCGCTGTCTTCTGTAAAAATTGCTATGAGAGAACTTTTCACTCACTGTTTTGCAGTTT
CTCCCTCAGTCCCTGGTTCTTCTTCTCACATAATCCCAATTTCAATTTATAGTTCATGGCCCAGGCAGAGTCA
TTCATCACGGCATCTCCTGAGCTAAACCAGCACCTGCTGCTCACTTCTTGACTGGCTGCTCATCATCAGCCC
TCTTGCAGAGATTTCAATTCCTCCCGTGCCAGGTACTTCACGCACCAAGCTCA

Fig. 1M

14/101

13735.1

GGATAATGAAGTTGTTTTATTTAGCTTGGACAAAAAGGCATATTCTCTATTTTCTTATACAACAAATATCCCC
AAAATAAAGCAAGCATATATATCTTGAATGTGTAATAATCCAGTGATAAACAAGAGCAGTACTTTAAAAGAAAA
AAAAATATGTATTTCTGTCAGGTTAAAATGAGAATCAAAACCATTTACTCTGCTAACTCATTATTTTTTGCTTT
CTTTTTGGTTAAGAGAGGCAATGCAATACACTGAAAAAGGTTTTATCTTATCTGGCATTGGAATTAGACATAT
TCAAACCCAGCCCCCATTTCCAAACCTTTAAGACCACAAACAAGTAATTTACTTTTCTGAACATTGGTTTTTTC
TGGAAAATGGGAATTATAAAATAGACTTTGCAGACTCTTATGAGATTAATAAGATAATGTATGAAATTCTTTC
TTCTTTTTTACTTCTTTTTCTTTTTGAGATGGAGTCTCACCCCGTCACCCAGGCTGGAGTACAGTG

13735.2

CCACTGCACTCCAGCCTGGGTGACGGAGTGAGACTCTGTCTCAAAAAACAAACAAACAAACAAAAAACT
GAAAAGGAAATAGAGTTCCTCTTCTCATATATGAATATATTATTTCAACAGATTGTTGATCACCTACCATAT
GCTTGGTATTGTTCTAATTGCTGGGGATACAGCAAGAGGTTCTGCAGAACTTCATGGAGCATGAAAGTAAATAA
ACAAAGTTAATTTCAAGGCCAGGCATGGTTGCTCACACCTTTAGTCCCAGCACTTTGGGAGGCTGAGGCAGGTG
GATCACTTGGGCCCAGGAGTTCAAGGCTGCAGTGAGCCAAGATTGTGCCACTACTCTCCAGGCTGGGCAACAGA
GCAAGACCCTGTCTCAGGGGGAACAAAAAGTTAATTTAGATTTTGTAAAGTGCTGTAAAGGAAGTAAATAGGT
TGATATTCAAGAGAGCACCTGAAGGCCAGGCGTGGTGGCTCACGCCTGTGGTCTAACGCTTTGGGAAGCCCGAG
CGGGCGGATCACAAGGTCAGGAGAATTTTGGCCAGGCATGGTG

13736.1

AGAATCCATTTATTGGGTTTTAACTAGTTACACAACCTGAAATCAGTTTGGCACTACTTTATACAGGGATTACG
CCTGTGTATGCCGACACTTAAATACTGTACCAGGACCACTGCTGTGCTTAGGTCTGTATTAGTCATTACGCAT
GTAGATACTAAAAATATACTGTAGTGTTCTTTAAGGAAGACTGTACAGGGTGTTGCAAGATGACATTACCC
AATTTGTGAATTATTTCAACCCAGAAGATACCTTTCACTCTATAAACTTGTATAGGCAACATGTGGTGTTAG
CATTGAGAGATGCACACAAAAATGTTACATAAAAGTTCAGACATTCTAATGATAAGTGAAGTGAACAAAAA
AACCCACATCTCAATTTTTGTAACAAGATAAAGAAAAATTTTAAAAACAAAAAATGGCATTAGTGGGTGTA
CAAAGCC

13737.1&2

CAAATATTTAATATAAATCTTTGAAACAAGTTCAGAKGAAATAAAAAATCAAAGTTTGCAAAAACGTGAAGATTA
ACTTAATTGTCAAATATTCCTCATTGCCCCAAATCAGTATTTTTTTTATTTCTATGCAAAAGTATGCCTTCAAA
CTGCTTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCATCTTGCAATTGTAAG
AAATAGGTAAAAGATTATAAGACACCTTACACACACACACACACACACACAGTGTGCACcGCCAATGAC
AAAAACAATTTGGCCTCTCCTAAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGGGAACACTGTGTCA
CCCCTCCCTACAATCCAGGTAGTTTCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGTGATTCTGA
CAGCCACSGTTGAAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGCCCTGAAAAAATGCCAATAATTTT
TCGCTCCCACCTTCTGCTGCTGTCTCTCCACATCCTACATAGACCCAGACCCGCTGGCCCCCTGGCTGGGCAT
CGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTACAGAAGCGATACACCAAATTGCCTGGTCGG
TCATTGTCATAACCAAG

Fig. 1N

15/101

13738.1

TTTGACTTTAGTAGGGGTCTGAACTATTTATTTTACTTTGCCMGTAATATTTARACCYTATATATCTTTCATTA
TGCCATCTTATCTTCTAATGBCAAGGGAACAGWTGCTAAMCTGGCTTCTGCATTWATCACATTA AAAATGGCTT
TCTTGGAAAATCTTCTTGATATGAATAAAGGATCTTTTAVAGCCATCATTTAAAGCMGGNTTCTCTCCAACACG
AGTCTGCTASASGGGGGKGAGCTGTGAACTCTGGCTGAAGGCTTTCCCATACACACTGCAATGACMTGGTTTCT
GACCAGBGTGAGTTA

13738.2

AGAGAAGCCCCATAAATGCAATCAGTGTGGGAAGGCCCTTCAGTCAGAGCTCAAGCCTTTTCTCCATCATCGGG
TTCATACTGGAGAGAAAACCTATGTATGTAATGAATGCCGCGAGAGCCTTTGGTTTTAACTCTCATCTTACTGAA
CACGTAAGGATTCACACAGGAGAAAAACCTATGTTTGTAATGAGTGCGGCAAAGCCTTTCTGTCGGAGTTCCAC
TCTTGTTGAGCATCGAAGAGTTCACACTGGGGAGAAGCCCTACCAAGTGCCTTGAATGTGGGAAAGCTTTCAGCC
AGAGCTCCCAGCTCACCTACATCAGCCGAGTTCACACTGGAGAGAAGCCCTATGACTGTGGTGACTGTGGGAA
GGCCTTCAGCCGGAGGTCAACCCTCATTGAGCATCAGAAAGTTCACAGCGGAGAGACTCGTAAGTGCAGAAAAC
ATGGTCCAGCCTTTGTTTCATGGCTCCAGCCTCACAGCAGATGGACAGATTCCCACTGGAGAGAAGCACGGCAGA
ACCTTTAACCATGGTGCAAATCTCATTCTGCGCTGGACAGTTC

13739.1&2

GAGACAGGGTCTCACTTTGTCAACCAGGCTGGAATGCAGTGGTGCGATCTTACGTAGCTCACTGCAGCCCTGAC
CTCCTGGACTCAAACAATTCTCCTGCCTCAGCCCTGCAAGTAGCTGGGACTGTGGGTGCATGCCACCATGCCTG
GCTAACTTTTGTAGTTTTTGTAAAGATGGGGTTTTGCCATGTTGCACATGCTGGTCTTGAACCTCTGAGCTCAA
ACGATCTGCCACCTCGGCCTCCAGAATGTTGGGATTACAGGGGTAAACCACCACGCCTGGCCCCATTAGGGT
ATTCTTAGCATCCACTTGCTCACTGAGATTAATCATAAGAGATGATAAGCACTGGAAGAAAAAATTTTTACTA
GGCTTTGGATATTTTTTCTTTTTTCAGCTTTATACAGAGGATTGGATCTTTAGTTTTCTTTAACTGATAATA
AAACATTGAAAGGAAATAAGTTTACCTGAGATTACAGAGATAACCGGCATCACTCCCTTGCTCAATTCCAGTC
TTTACCACATCAATTATTTTCAGAGGTGCAGGATAAAGGCCCTTAGTCTGCTTTCGCACTTTTTCTTCCACTTT
TTTGTAACCTGTTGCCTGACAAATGGAATTGACAGCGTATGCCATGACTATTCCATTTGTGAGGCATACGCTG
TCAATTTTTCCACCAATCCCTTGTCTCTTTGGAGAGATCTTCTTATCAGCTAGTCCTTTGGCAAAAGTAATT
GCAACTTCTTCTAGGTATTCTATTGTCCGTTCCACTGGTGGAAACCCTGGGACCAGGACTAAAACCTCCAG

13741.1

ATCTCATATATATATTTCTTCTGACTTTATTTGCTTGCTTCTGNCACGCATTTAAAATATCACAGAGACCAAA
ATAGAGCGGCTTTCTGGTGGAACGCATGGCAGTCACAGGACAAAATACAAAACCTAGGGGGCTCTGTCTTCTCAT
ACATCATACAATTTTCAAGTATTTTTTTATGTACAAAGAGCTACTCTATCTGAAAAAAATTA AAAAATAAAT
GAGACAAGATAGTTTATGCATCCTAGGAAGAAAGAATGGGAAGAAAGAACGGGGCAGTTGGGTACAGATTCTG
TCCCTGTTCCAGGGACCACTACCTTCTGCCACTGAGTTCCCCACAGCCTCACCCATCATGTACAGGGCA
AGTGCCAGGGTAGGTGGGGACCAGTGGAGACAGGAACCAGCAACATACTTTGGCCTGGAAGATAAGGAGAAAGT
CTCAGAAACACACTGGTGGGAAGCAATCCACNGGCCGTGCCCCANGAGCTTCCACCTGCTGCTGGCTCCCTG
GGTGGCTTTGGGAACAGCTTGGGCAGGCCCTTTGGGTGGGGNCCAACCTGGGCCTTTGGGCCGTGTGGAAAG

Fig. 10

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13742.1

AAACATTGAGATGGAATGATAGGGTTTCCCAGAATCAGGTCCATATTTTAACTAAATGAAAATTATGATTTATA
GCCTTCTCAAATACCTGCCATACCTTGATATCTCAACCAGAGCTAATTTTACCTCTTTACAAATTAATAAGCAA
GTAAGTGGATCCACAATTTATAATACCTGTCAATTTTTCTGTATTAAACCTCTATCATAGTTTAAGCCTATTA
GGGTACTTAATCCTTACAAATAAACAGGTTTAAATCACCTCAATAGGCAACTGCCCTTCTGGTTTTCTTCTTT
GACTAAACAATCTGAATGCTTAAGATTTTCCACTTTGGGTGCTAGCAGTACACAGTGTTACACTCTGTATTCCA
GACTTCTTAAATTATAGAAAAAGGAATGTACACTTTTTGTATTCTTTCTGAGCAGGGCCGGGAGGCAACATCAT
CTACCATGGTAGGGACTTGTATGCATGGACTACTTTA

14351.1

ACTCTGTCGCCCAGGCTGGAGCCCABTGGMGCGATCTCGACTCCCTGCAAGCTMCGCCTCACAGGWTGATGCCA
TTCTCCTGCCTCAGCATCTGGAGTAGCTGGGACTACAGGCGCCAGCCACCATGCCAGCTAATTTTT

14351.2

ACCTTAAAGACATAGGAGAATTTATACTGGGAGAGAAAGCTTACAAATGTAAGGTTTCTGACAAGACTTGGGAG
TGATTCACACCTGGAACAACATACTGGACTTCACACTGGABAGAAACCTTACAAGTGTAATGAGTGTGGCAAAG
CCTTTGGCAAGCAGTCAACACTTATTCACCATCAGGCAATTCA

14354.2

AGTCAGGATCATGATGGCTCAGTTTTCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAAG
AACGTACTAAGCATGATAACAGTTTGATAACCTCAAACCTTCAGGAGGTTACATAACAGGTGATCAAGCCCGT
ACTTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAATATGGGCCTTATCAGATCTGAACAAGGA
TGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAACTCATCAAGTTAAAGTTGCAGGGCCAAACAGCTGC
CTGTAGTCCCTCCCTATCATGAAACAACCCCTATGTTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGA
AGCATGCCAATCTGTCCATTATCAGCCATTGCCTCCAGTTGCACCTATAGCAACACCCTGTCTCTGCTAC
TTCAGGGACCAGTATTCCTCCCTAATGATGCCTGCT

14354.1

CTTTGATTTCTTCAATTTGTCACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTATTATAGCT
TTCTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTTTCAAGAG
CATCTAATTGTTCTTTAAGTCTTTGGCATAATTCTTCTTTCTGATGACTTTCTATGAAGTAACTGATCCCT
GAATCAGGTGTGTTACTGAGCTGCATGTTTTAATTCTTTGTTTAAAGCTGCTTCTCAGGGACCAGATAGAT
AAGCTTATTTTGATATTCCTTAAGCTCTTGGTGAAGTTGTTGATTTCCATAATTTCCAGGTCACACTGGTTAT
CCCAAACCTTCT

Fig. 1P

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16431.1.2

GTGGAGGTGAAACGGAGGCAAGAAAGGGGGCTACCTCAGGAGCGAGGGACAAAGGGGGCGTGAGGCACCTAGGC
CGCGGCACCCCGGCACAGGAAGCCGTCTGAACCGGGCTACCGGGTAGGGGAAGGGCCCGGTAGTCCTCGCA
GGGCCCCAGAGCTGGAGTCGGCTCCACAGCCCCGGGCGTCGGCTTCTCACTTCCTGGACCTCCCCGGCGCCCG
GGCCTGAGGACTGGCTCGGCGGAGGGAGAAGAGGAACAGACTTGAGCAGCTCCCCGTTGTCTCGCAACTCCAC
TGCCGAGGAACTCTCATTTCTTCCCTCGCTCCTTACCCCCACCTCATGTAGAAAGGTGCTGAAGCGTCCGGA
GGGAAGAAGAACCTGGGCTACCGTCTGGCCTTCCMCCCCCTTCCCGGGCGCTTTGGTGGGCGTGAGTTGG
GGTTGGGGGGGTGGGTGGGGTTCTTTTTGGAGTGTGGGGAACCTTTTTCCCTTCTTCAGGTGAGGGGAAAG
GGAATGCCAATTGAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAACCTTGCAGCCGTC
ATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCGAAGCACAAGCGGCATAAGTCCAAAC
ACTCCAAAGACATGGGGTTGGTGACCCCGAAGCAGCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTAT
GATGATATCAGCTCTGATTCCGACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGA
ACGTCGTGGATCAGATCGGAGCGACCGCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGGGACTTAC
TAAAAGCTAAACAGACCG

16432-1

GACATGTTTGCTGCAGGGGACCAGAGACAATGGGATTAGCCAGTGCTCACTGTTCTTTATGCTTCCAGAGAGG
ATGGGGACAGCTCTCAGGTCAGAATCCAGGCTGAGAAGGCCATGCTGGTTGGGGGCCCCCGAAGCACGGTCCG
GATCCTCCCTGGCATCAGCGTAGACCGCTGCTCAGGCTTGGGGTACCAAACCTCATGCTCTGTACTGTTTTGGC
CCCATGCGGTGAGAGGAAAACCTAGAAAAAGATTGGTCGTGCTAAGGAATCAGCTGCCCCCTCATCTCCGCAT
CCAATGCTGGTGACAACATATTCCTCTCCCAGGACACAGACTCGGTGACTCCACACTGGGCTGAGTGGCCTCT
GGAGGCTCGTGGCCTAAGGCAGGGCTCCGTAAGGCTGATCGGCTGAACCTGGGTGGGGTGAGGGTTTCTGACCT
TCGCTTCCCATCCATAACCGCTGTCAATGAGCTCACACTGTGGTCA

16432-2

GATGGCATGGTCGTTGCTAATGTGCCTGCTGGGATGGAGCACTTCCTCCTGTGAGCCAGGGGACCCGCTGTC
CCTGGAGCTTGGGGCAAGGAGGGAAGAGTGATACCAGGAAGGTGGGGCTGCAGCCAGGGGCCAGAGTCAGTTCA
GGGAGTGGTCCTCGGCCCTCAAAGCTCCTCCGGGGACTGCTCAGGAGTGATGGTGCCCTGGAGTTTGGCCCAAC
TTCCCTGGCCACCCTGGAAGGTGCCTGGCTGCTCAGGCTCTAGGCTGGGCTGATGGGTTTCTCCAGGACACA
AGTATCATTAAGCCACCCTCTCCTCAGCTTGTCAGGCCGCACATGTGGGACAGGCTGTGCTCACAACCCCTC
GCCTGCCCTGCCCTCCATCAGGAGGAGCCAGTGGAACCTTCGGAAGCTCCAGCATCTCAGCAGCCCTCAAAA
GTGTCCTGGGGCAAGCTCTGGTTCTCCTGACTGGAGGTATCTGGGCTTGGCCTGCTCTCTCGC

17184.3

TAAAAAGTGTAACAAAGGTTTATTTAGACTTTCTTCATGCCCCAGATCCAGGATGTCTATGTAAACGTTAT
CTTACAAAGAAAGCACAAATATTTGGTATAAACTAAGTCAGTGACTTGCTTAACTGAAATAGCGTCCATCAAAA
GTGGGTTTAAAGTAAACTACCTGACGATATTGGCGGGGATCCTGCAGTTTGGACTGCTTGCCGGGTTTGTCCA
GGGTTCCGGGTCTGTTCTTGGCACTCATGGGACAGGCATCCTGCTCGTCTGTGGGGCCCCGCTGGAGCCCTTA
CGTGAAGCTGAAGGTATCGACCSTAGGGGGCTCTAGGGCAGTGGGACCTTCATCCGGAACCTAACAGGGTCGGG
GAGAGGCCTCTTGGGCTATGTGGG

Fig. 1Q

18/101

17184.4

CAAGCGTTCCTTTATGGATGTAATTCAAACAGTCATGCTGAGCCATCCCGGGCTGACAGTCACGTTWAAGACA
CTAGGTCGGGCGCCACAGTGCCACCCAAGGAGAAGAAGAAATTTGGAATTTTCCATGAAGATGTACGGAAATCT
GATGTTGAATATGAAAATGGCCCCAAATGGAATTCAAAAGGTTACCACAGGGGCTGTAAGACCTAGTGACCC
TCCTAAGTGGGAAAGAGGAATGGAGAATAGTATTTCTGATGCATCAAGAACATCAGAATATAAACTGAGATCA
TAATGAAGGAAAATTCATATCCAATATGAGTTTACTCAGAGACAGTAGAACTATTCCCAGG

17185.1

TAGGAATAACAAATGTTTATTAGAAATGGATAAGTAATACATAATCACCTTCATCTCTTAATGCCCTTCCT
CTCCTTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGGAGGAGGACACAGGACTAGCCAC
CACCTTCTCTCCCGGTCTCCAAGATGACTGCTTATAGAGTGGAGGAGGCAAACAGGTCCCTCAATGTACCA
GATGGTCACCTATAGCACCAGCTCCAGATGGCCACGTGGTTGCAGCTGGACTCAATGAACTCTGTGACAACCA
GAAGATACCTGCTTTGGGATGAGAGGGAGGATAAAGCCATGCAGGGAGGATATTTACCATCCCTACCCTAAGCA
CAGTGCAAGCAGTGAGCCCCGGCTCCAGTACCTGAAAAACCAAGGCCTACTGNCTTTTGATGCTCTCTTG
GCCACG

17188.2

AAGCCTCCTGCCCTGGAAATCTGGAGCCCCCTGGAGCTGAGCTGGACGGGGCAGGGAGGGGCTGAGAGGCAAGA
CCGTCTCCCTCCTGCTGCAGCTGCTTCCCCAGCAGCCACTGCTGGGCACAGCAGAAACGCCAGCAGAGAAAATG
GGAGCCGAGAGTCCTTAGCCCTGGAGCTGAGGCTGCCTCTGGGCTGACCCGCTGGCTGTACGTGGCCAGAACTG
GGGTTGGCATCTGGCATCCATTTGAGGCCAGGGTGGAGGAAAGGGAGGCCAACAGAGGAAAACCTATTCTGCT
GTGACAACACAGCCCTTGTCACGCAGCCTAAGTGCAGGGAGCGTGATGAAGTCAGGCAGCCAGTCGGGGAGG
ACGAGGTAACCTCAGCAGCAATGTCACCTTGAGCCTATGCGCTCAATGGCCCGGAGGGGCAGCAACCCCCGCA
CACGTCAGCCAACAGCAGTGCTCTGCAGGCACCAAGAGAGCGATGATGGACTTGAGCGCCGTGTTT

17190.1

GTTTGGCAGAAGACATGTTTAATAACATTTTCATATTTAAAAAATACAGCAACAATTCTCTATCTGTCCACCAT
CTTGCCCTTGCCCTTCTGGGGCTGAGGCAGACAAAGGAAAGGTAATGAGGTTAGGGCCCCAGGCGGGCTAAGT
GCTATTGGCCTGCTCCTGCTCAAAGAGAGCCATAGCCAGCTGGGCACGGCCCCCTAGCCCCCTCAGGTTGCTGA
GGCGGCAGCGGTGGTAGAGTTCTTCACTGAGCCGTGGGCTGCAGTCTCGCAGGGAGAACTTCTGCACCAGCCCT
GGCTCTACGGCCCGAAAGAGGTGGAGCCCTGAGAACCAGGAGGAAAACATCCATCACCTCCAGCCCCCTCAGGGC
TTCTCTCTTCTGCGCTGCCAGTTCACCTGCCAGCCGGGCTCGGGCCGCCAGGTAGTCAGCGTTGTAGAAGC
AGCCCTCCGAGAAGCCTGCCGGTCAAATCTCCCCGTATAGGAGCCCCCGGAGGGGTCAGCACC

Fig. 1R

19/101

17190.2

CAAGTTGAACGTCAGGCTTGGCAGAGGTGGAGTGTAGATGAAAACAAAGGTGTGATTATGAAGAGGATGTGAGT
CCTTTGGGTGTAGGAGAGAAAGGCTGTTGAGCTTCTATTTCAAGATACTTTTACCTGTGCAAAAAGCACATTTT
CCACCTCCTTCTCATGGCATTGTGTAAAGGTGAGTATGATTCTATTCCATCTGCATTTTAGAGGTGAAGAATA
ACGTACAAGGGATTGAGTATTAGCAAGGGACCCCTCACTAAGTGTTGATGGAGTTAGGACAGAGCTCAGCTGT
TTGAATCTCAGAGCCCAGGCAGCTGGAGCTGGGTAGGATCCTGGAGCTGGCACTAATGTGAGGTGCATTCCCTC
CAACCCAGGCTCAGATCCGGAACCTGACCGTGCTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGG
CTCCCTGCTCCTTTCACACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGC

17191.2&89.2

TGGCCTGGGCAGGATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTATGACC
CCATCATTTCCCAGAGGTCTCGGCCTCCTTTGGTGTTGAGCAGCTGCCCCTGGAGGAGATCTGGCCTCTCTGT
GATTTCACTACTGTGCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCAGTG
CAAGAAGGGGGTGCGTGTGGTGAACGTGCCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGCCCTGC
AGTCTGGCCAGTGTGCCGGGGCTGCACTGGACGTGTTACGGAAGAGCCGCCACGGGACCGGGCCTTGGTGGAC
CATGAGAATGTCATCAGCTGTCCCCACCTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAAT
TGCTGTTGAGTTCGTGGACATGGTGAAGGGGAAATCTCTACGGGGGTTGTGAATGCCAGGCCCTT

Fig. 1S

20/101

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGG
CCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGG
AGGTTACATAACAGGTGATCAAGCCCGTACTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAA
TATGGGCCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATC
AAGTTAAAGTTGCAGGGCCAAACAGCTGCCTGTAGTCCTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCC
ACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCAATCTGTCCATTCATCAGCCATTGCCTCCAGTTGCAC
CTATAGCAACACCCTTGCTTCTGCTACTTCAGGGACCAGTATTCTCCCTAATGATGCCTGCTCCCTAGTG
CCTTCTGTTAGTACATCCTCATTACCAAATGGAAGTCCAGTCTCATTACAGCCTTTATCCATTCTTATTCTTC
TTCAACATTGCCTCATGCATCATCTTACAGCCTGATGATGGGAGGATTTGGTGGTGCTAGTATCCAGAAGGCCC
AGTCTCTGATTGATTTAGGATCTAGTAGCTCAACTTCCTCAACTGCTTCCCTCTCAGGGAAGTCACTAAGACA
GGGACCTCAGAGTGGGCAGTTCTCAGCCTTCAAGATTAAAGTATCGGCAAAAATTTAATAGTCTAGACAAAGG
CATGAGCGGATACCTCTCAGGTTTTCAAGCTAGAAATGCCCTTCTTCAGTCAAATCTCTCTCAAACCTCAGTAG
CTACTATTTGGACTCTGGCTGACATCGATGGTGACGGACAGTTGAAAGCTGAAGAATTTATTCTGGCGATGCAC
CTCACTGACATGGCCAAAGCTGGACAGCCACTACCACTGACGTTGCCTCCCGAGCTTGCTCCCTCCATCTTTCAG
AGGGGGAAAGCAAGTTGATTCTGTTAATGGAAGTCTGCCTTCATATCAGAAAACACAAGAAGAAGAGCCTCAGA
AGAAACTGCCAGTTACTTTTGAGGACAAACGGAAAGCCAACTATGAACGAGGAAACATGGAGCTGGAGAAGCGA
CGCCAAGTGTTGATGGAGCAGCAGCAGAGGGAGGCTGAACGCAAAGCCCAGAAAGAGAAGGAAGAGTGGGAGCG
GAAACAGAGAGAACTGCAAGAGCAAGAATGGAAGAAGCAGCTGGAGTTGGAGAAACGCTTGGAGAAACAGAGAG
AGCTGGAGAGACAGCGGGAGGAAGAGAGGAGAAAGGAGATAGAAAGACGAGAGGCAGCAAAACAGGAGCTTGAG
AGACAACGCCGTTTGAATGGGAAAGACTCCGTCCGGCAGGAGCTGCTCAGTCAGAAGACCAGGGAACAAGAAGA
CATTGTCAGGCTGAGCTCCAGAAAGAAAAGTCTCCACCTGGAAGTGAAGCAGTGAATGGAAAACATCAGCAGA
TCTCAGGCAGACTACAAGATGTCCAAATCAGAAAGCAAACACAAAAGACTGAGCTAGAAGTTTTGGATAAACAG
TGTGACCTGGAAATTATGGAAATCAAACAACCTTCAACAAGAGCTTAAGGAATATCAAAATAAGCTTATCTATCT
GGTCCCTGAGAAGCAGCTATTAACGAAAGAATTAATAACATGCAGCTCAGTAACACACCTGATTCAGGGATCA
GTTTACTTCATAAAAAGTCATCAGAAAAGGAAGAATTATGCCAAAGACTTAAAGAACAATTAGATGCTCTTGAA
AAAGAACTGCATCTAAGCTCTCAGAAATGGATTCAATTAACAATCAGCTGAAGGAACTCAGAGAAAGCTATAA
TACACAGCAGTTAGCCCTGAACAACTTCATAAAATCAAACGTGACAAATTGAAGGAAATCGAAAGAAAAAGAT
TAGAGCAAAAAAAAAAAAA

Fig. 2A

21/101

ATGGCAGTGACATTACCATCATGGGAACCACTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCACC
CAGTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGT
GCCAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAACTTTCTAA
CTTCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAAGTGGTGTTA
CCCAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAAACAGGATGTGCTTTCCTTTGC
CCATTTAGGGTTTCTTCTTTCCCTTTCTTTTATTAACCACTA

Fig. 2B

22/101

ATATCTAGAAGTCTGGAGTGAGCAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGA
ACAAGATAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTAA
GAGTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGG
GGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTATGTTATATGTGCTGTAATGTTGCTCTGA
GGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTAGTATGTACCCTA
AGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTT
TTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATA
ATTTTAGCATAAACAGAGCAGTCGGCGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAACAA
ATGCGGGTTTATTTCTCAGATGATGTTTCATCCGTGAATGGTCCAGGGAAGGACCTTTCACCTTGACTATATGGC
ATTATGTCATCACAAGCTCTGAGGCTTCTCCTTTCATCCTGCGTGGACAGCTAAGACCTCAGTTTTCAATAGC
ATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGGAATGTCTGAAGACAATTTTGTT
ACCTCAATGAGGGAGTGGAGGAGGATACAGTGCTACTACCAACTAGTGGATAAAGGCCAGGGATGCTGCTCAAC
CTCCTACCATGTACAGGACGTCTCCCCATTACAACACCAATCCGAAGTGTCAACTGTGTCAGGACTAAGAAA
CCCTGGTTTTGAGTAGAAAAGGGCCTGGAAGAGGGGAGCCAACAAATCTGTCTGCTTCTCACATTAGTCATT
GGCAAATAAGCATTCTGTCTCTTTGGCTGCTGCCTCAGCACAGAGAGCCAGAAGTCTATCGGGCACCAGGATAA
CATCTCTCAGTGAACAGAGTTGACAAGGCCTATGGGAAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTC
TAAGTTTCTTTCCCTTCATTCTACCCTGCAAGCCAAGTTCTGTAAGAGAAATGCCTGAGTTCTAGCTCAGGTTT
TCTTACTCTGAATTTAGATCTCCAGACCCTTCTGGCCACAATTCAAATTAAGGCAACAAACATATACCTTCCA
TGAAGCACACAGACTTTTGAAAGCAAGGACAATGACTGCTTGAATTGAGGCCTTGAGGAATGAAGCTTTGAA
GGAAAAGAATACTTTGTTCCAGCCCCCTTCCCACACTTTCATGTGTTAACCCTGCCTTCTGGACCTTGGA
GCCACGGTGACTGTATTACATGTTGTTATAGAAAAGTATTTAGAGTTCTGATCGTTCAAGAGAATGATTAAA
TATACATTTCCCTA

Fig. 2C

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Element Display											
Off Exp	Probe 1	Exp	Probe 2	Gene/Element	Probe Name	Probe 1	S/B	A2	Probe 2	S/B	A2
+1.7	384A Ovary T (nests)	C	272A Dendritic cells	422A0608 (420)	421G0196 (C11)	2993	19.1	69	1430	2.0	50
-1.1	335A Ovary T		S7 Ovary N	422G0626 (420)	421G0196 (C11)	365	2.7	54	392	1.8	54
+1.8	261A Ovary T		S10 Skeletal muscle N	422G0621 (420)	421G0196 (C11)	1298	6.8	51	707	1.9	51
+8.1	284A Ovary T	C	S2 Pancreas N	422G0629 (420)	421G0196 (C11)	850	44.1	62	1180	2.3	62
-1.2	386A Ovary T		S40 PLMC (activated)	422G0605 (420)	421G0196 (C11)	516	3.8	60	618	2.0	60
+4.7	285A Ovary T	C	CT5 Heart N	422G0624 (420)	421G0196 (C11)	2305	14.1	53	489	2.2	53
-1.4	S25 Ovary T		CT4 Bone Marrow N	422H0619 (420)	421G0196 (C11)	531	3.5	63	743	2.0	53
	383A Ovary T (nests)		CT1 Colon N	422G0609 (420)	421G0196 (C11)	1842	10.1	58	671	2.0	39
-1.9	S22 Ovary T		CT9 Kidney N	422G0627 (420)	421G0196 (C11)	459	3.3	68	657	3.2	68
+3.2	3485 OT 1-P (SCID)	C	3485 OT 1-P (SCID)	422Y0602 (420)	421G0196 (C11)	1882	12.1	57	594	2.3	57
+1.5	262A Ovary T		334A Large Intestine N	422A0622 (420)	421G0196 (C11)	1486	7.5	55	965	2.2	55
-1.1	S115 Ovary T (nests)		CT10 Small Intestine N	422G0604 (420)	421G0196 (C11)	509	3.4	51	573	2.0	51
+1.1	288A Ovary T		CT12 Lung N	422Y0625 (420)	421G0196 (C11)	700	4.5	54	651	2.1	54
-2.1	201A Ovary T		S6 Stomach N	422A0620 (420)	421G0196 (C11)	625	4.6	46	1395	3.6	46
+7.8	S23 Ovary T	C	S56 Spinal Cord N	422G0626 (420)	421G0196 (C11)	3696	22.1	50	502	2.2	50
+1.8	265A Ovary T	C	270A Liver N	422Q0606 (420)	421G0196 (C11)	2251	14.1	46	1266	2.0	46
-1.9	333A Ovary T (SCID)		CT Skin N	422R0601 (420)	421G0196 (C11)	552	3.4	72	1029	2.3	72
+5.6	365A Ovary T	C	S31 Fetal tissue	422X0607 (420)	421G0196 (C11)	9126	35.1	50	1499	2.0	50
-3.5	263A Ovary T		S73 Breast N	422H0623 (420)	421G0196 (C11)	439	3.2	61	1531	3.4	61
-3.3	362A Ovary T		CT19 Brain N	422G0610 (420)	421G0196 (C11)	387	3.2	50	1278	2.1	50
+4.8	268A Ovary T	C	S27 Ovary N	422S0603 (420)	421G0196 (C11)	4242	22.1	58	883	2.0	58

Fig. 3

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TCGAGCGGCCGCCGGGCAGGTCCTTCAGACTTGGACTGTGTCACACTGCCAGGCTTCCAGGGCTCCAATTGC
AGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACACCATGGTT
TTATCCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATATTTCTAC
CTCGGCCGCGACCACGCT

Fig. 4

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TAGCGYGGTCGCGGCCGAGGYCTGCTTYTCTGTCCAGCCCAGGGCCTGTGGGGTCAGGGCGGTGGGTGCAGATG
GCATCCACTCCGGTGGCTTCCCCATCTTCTCTGGCCTGAGCAAGGTCAGCCTGCAGCCAGAGTACAGAGGGCC
AACTGGTGTTCCTTGAACAAGGGCCTTAGCAGGCCCTGAAGGCCCTCTCTGTAGTGTGAACTTCCTGGAGC
CAGGCCACATGTTCTCCTCATACCGCAGGYTAGYGATGGTGAAGTTGAGGGTGAAATAGTATTMANGRAGATGG
CTGGCARACCTGCCCGGGCGGCCGCTCSAAATCC

Fig. 5

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AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTGAGCTCTCTG
TACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCAC
CCATCGTCCTGACCCAAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACG
GCATCACTGAGCTGGGCCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCT
GTACCCACCACCAGCACCGGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

Fig. 6

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TTGGGGNTTTMGAGCGGCCGCCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACCTCACCA
TCAACAACCTGCGGTATGAGGAGAACATGCAGCACCCCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTT
CAGGGCCTGCTCAGGTCCCTGTTCAAGAGCACCACTGTTGGCCCTCTGTACTCTGGCTGCAGACTGACTTTGCT
CAGACTTGAGAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCTTGATCCCACTGGTCCTG
GACTGGACAGAGAGCGGCTATACTGGGAGCTGAGCCAGTCCTCTGGCGGNGACNCCNCTT

Fig. 7A

AGCGTGGTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCACTGGCACAGTGAGGAAGATCTCTG
CTGTCAGTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAAGTGATTTAATACACCTAACGTATCGAACAT
CATAGCTTGGCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCGGGCGGCCGC
TCGA

Fig. 7B

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TGTGGTGTTGAACTTCCTGGAGNCAGGGTGACCCATGTCCTCCCCATACTGCAGGTTGGTGATGGTGAAGTTGA
GGGTGAATGGTACCAGGAGAGGGCCAGCAGCCATAATTGTSGRGCKGSMGMSSGAGGMWGGWGTYYCWGAGGTT
CYRARRTCCACTGTGGAGGTCCCAGGAGTGCTGGTGGTGGGCACAGAGSTCYGATGGGTGAAACCATTGACATA
GAGACTGTTCTGTCCAGGGTGTAGGGGCCAGCTCTTYRATGYCATTGGYCAGTTKGCTYAGCTCCCAGTACA
GCCRCTCTCKGYYGWCCAGSGCTTTTGGGGTCAAGATGATGGATGCAGATGGCATCCACTCCAGTGGCTGCT
CCATCCTTCTCGGACCTGAGAGAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTTCTTTGAATA

Fig. 8

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TCGAGCGGCCGCGGGCAGGTCAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCACCTGTGCTG
CGGACATCTCCAGGGAGTGCAGAAGGGAAGCAGGTCAAACCTGCTCAGATCAGTCAGACTGGCTGTTCTCAGTTC
TCACCTGAGCAAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTTCCTGAACAAGGGCTTGAGCA
GACCCTGCAGAACCCCTCTCCGTGGTGTGAACTTCCTGGAAACCAGGGTGTTCATGTTTTCTCATAATGC
AAGGTTGGTGATGG

Fig. 9

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Gene Name	Ref. Probe 1	P1	P2 Name	Probe 2	Probe 1	Probe 2	Probe 1	Probe 2	Probe 1	Probe 2
Name	Exp. Name			Value	Value	S/B	S/B	AN	AN	AN
42100188 (D3)	+1.0 205A Ovary T	270A Liver N	422Q0606	8620	1240	57.7	65	2.2	65	65
42100188 (D3)	+5.9 323 Ovary T	536 Spinal Cord N	422G0628	5894	1002	35.3	89	3.9	89	89
42100188 (D3)	+5.7 385A Ovary T	591 Fetal tissue	422X0607	12151	2121	54.3	73	2.8	73	73
42100188 (D3)	+5.1 426A Ovary T (met)	415A Aorta N	422X0611	7487	1480	53.0	73	9.7	73	73
42100188 (D3)	+3.5 263A Ovary T	573 Breast N	422H0623	7302	2116	39.2	84	4.5	84	84
42100188 (D3)	+3.3 383A Ovary T (met)	11 Colon N	422B0609	3714	1113	20.4	83	2.6	83	83
42100188 (D3)	+3.0 933A Ovary T (SCD)	12 Skin N	422R0601	2435	814	12.1	75	2.1	75	75
42100188 (D3)	+2.6 384A Ovary T (met)	272A Dendritic cell	422A0608	4578	1754	25.0	69	2.3	69	69
42100188 (D3)	+2.2 264A Ovary T	52 Pancreas N	422N0629	7904	5595	38.5	81	5.6	81	81
42100188 (D3)	+2.0 386A Ovary T	840 PBMC Yacciv	422J0605	2191	1081	14.0	90	2.9	90	90
42100188 (D3)	+2.0 5115 Ovary T (met)	CT10 Small intestine	422C0604	1979	971	10.4	80	2.7	80	80
42100188 (D3)	+2.0 265A Ovary T	CT5 Heart N	422O0624	1911	964	13.9	93	3.4	93	93
42100188 (D3)	+2.0 335A Ovary T	57 Ovary N	422A0625	1666	817	9.8	100	3.0	100	100
42100188 (D3)	+1.9 428A Ovary T (met)	243A Esophagus N	422A0612	1837	3480	19.4	97	9.5	97	97
42100188 (D3)	+1.6 261A Ovary T	510 Skeletal muscle	422J0621	5914	3653	30.4	86	6.0	86	86
42100188 (D3)	+1.6 266A Ovary T	527 Ovary N	422J0603	2039	1274	11.9	50	2.6	50	50
42100188 (D3)	+1.6 822 Ovary T	CT9 Kidney N	422B0627	1736	1072	11.0	92	4.9	92	92
42100188 (D3)	+1.4 9485 OT 1-P (SCD)	9485 OT 5-P (SCD)	422Y0602	4204	3074	23.0	93	7.7	93	93
42100188 (D3)	+1.4 262A Ovary T	334A Large Intestine	422A0622	3002	2101	16.6	89	4.0	89	89
42100188 (D3)	+1.3 525 Ovary T	CT4 Bone Marrow	422H0619	1623	1297	9.6	90	3.1	90	90
42100188 (D3)	+1.2 429A Ovary T (met)	364A Ovary N	422J0614	2521	2084	22.0	65	23.9	65	65
42100188 (D3)	+1.2 382A Ovary T	CT19 Brain N	422Q0610	2072	1663	10.9	88	2.3	88	88
42100188 (D3)	+1.2 288A Ovary T	CT12 Lung N	422Y0625	1840	1473	10.7	87	3.8	87	87
42100188 (D3)	+1.1 201A Ovary T	56 Stomach N	422Y0620	1329	1204	9.1	90	3.5	90	90

Fig. 10

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Gene Name	Seq Probe 1	P1	P2 Name	Probe 2	GEN ID	Probe1 Value	Probe2 Value	Probe1 S/B	Probe2 S/B	Probe1 A/V	Probe2 A/V
421B0181 (C3)	+18.8 385A Ovary T	⊙	S91 Fetal tissue		422X0607	26711	1424	103.3	2.0	54	54
421B0181 (C3)	+11.5 S23 Ovary T	⊙	S56 Spinal Cord N		422G0628	13559	1179	65.3	3.9	68	68
421B0181 (C3)	+11.1 426A Ovary T (meis)	⊙	415A Adip N		422X0611	14125	1273	67.3	5.6	61	61
421B0181 (C3)	+10.8 205A Ovary T	⊙	270A Liver N		422Q0606	16121	1483	93.3	2.3	43	43
421B0181 (C3)	+5.1 263A Ovary T	⊙	S73 Breast N		422H0623	11326	2235	58.2	4.4	68	68
421B0181 (C3)	+4.6 384A Ovary T (meis)	⊙	272A Dendritic cells		42240608	6583	1424	24.5	2.1	40	40
421B0181 (C3)	+4.4 264A Ovary T	⊙	S2 Pancreas N		422N0629	9865	2245	40.9	3.6	64	64
421B0181 (C3)	+4.4 429A Ovary T (meis)	⊙	364A Ovary N		422I0614	2803	638	22.6	7.4	60	60
421B0181 (C3)	+4.2 261A Ovary T	⊙	S10 Skeletal muscle		42230621	8271	1949	39.5	3.6	68	68
421B0181 (C3)	+3.8 -8115 Ovary T (meis)	⊙	CT10 Small Intestine		422C0604	2281	607	11.6	2.1	60	60
421B0181 (C3)	+2.5 265A Ovary T	⊙	CT5 Heart N		422O0624	3192	1293	19.2	4.0	68	68
421B0181 (C3)	-2.3 S22 Ovary T	⊙	CT9 Kidney N		42290627	565	1276	3.6	3.9	70	70
421B0181 (C3)	+2.2 266A Ovary T	⊙	S27 Ovary N		42250603	2774	1260	14.3	2.7	46	46
421B0181 (C3)	+2.1 9394 Ovary T (SCID)	⊙	12 Skin N		422R0601	1774	837	8.4	2.1	56	56
421B0181 (C3)	+1.9 9485 OT 1-P (SCID)	⊙	9485 OT 5-P (SCID)		422Y0602	6967	3726	41.5	70	9.2	70
421B0181 (C3)	+1.6 382A Ovary T	⊙	CT19 Brain N		422Q0610	2313	1471	6.2	1.9	50	50
421B0181 (C3)	+1.6 288A Ovary T	⊙	CT12 Lung N		422V0625	1657	1054	9.7	2.9	69	69
421B0181 (C3)	-1.5 S25 Ovary T	⊙	CT4 Bone Marrow N		422H0619	848	1243	4.5	65	65	65
421B0181 (C3)	+1.4 262A Ovary T	⊙	374A Large Intestine		422A0622	3171	2214	16.8	3.8	69	69
421B0181 (C3)	+1.2 886A Ovary T	⊙	S40 PBMC (activated)		422J0605	630	544	4.2	1.9	53	53
421B0181 (C3)	-1.2 335A Ovary T	⊙	S7 Ovary N		42220626	592	730	3.7	2.6	75	75
421B0181 (C3)	-1.0 201A Ovary T	⊙	S6 Stomach N		422V0620	1197	1237	7.8	3.5	65	65
421B0181 (C3)	-1.0 428A Ovary T (meis)	⊙	243A Esophagus N		42240612	783	797	4.5	2.4	95	95
421B0181 (C3)	383A Ovary T (meis)	⊙	11 Colon N		422B0609	3470	862	8.9	1.7	24	24

Fig. 11

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Gene Name	Ref. Probe 1	P1	P2 Name	Probe 2	GEM ID	Probe 1 Value	Probe 2 Value	Probe 1 S/B	Probe 2 S/B	Probe 1 AS	Probe 2 AS
42110182 (H7)	+16.7 426A Ovary T (met)	42110182 (H7)	415A Aorta N	422X0611	7705	462	46.3	75	3.5	75	75
42110182 (H7)	+10.7 205A Ovary T	42110182 (H7)	270A Liver N	422Q0606	10171	950	61.2	41	1.8	41	41
42110182 (H7)	+9.9 385A Ovary T	42110182 (H7)	S91 Regl disc	422X0607	14415	1459	62.1	48	2.2	48	48
42110182 (H7)	+8.8 523 Ovary T	42110182 (H7)	S56 Spinal Cord N	422G0628	7781	880	47.3	73	3.4	73	73
42110182 (H7)	+6.4 383A Ovary T (met)	42110182 (H7)	H1 Colon N	422B0609	4807	748	27.6	47	2.2	47	47
42110182 (H7)	+5.1 263A Ovary T	42110182 (H7)	S73 Breast N	422H0623	9815	1969	57.1	74	4.2	74	74
42110182 (H7)	+4.9 429A Ovary T (met)	42110182 (H7)	364A Ovary N	422H0614	2661	543	20.3	61	6.7	61	61
42110182 (H7)	+3.5 264A Ovary T	42110182 (H7)	S2 Pancreas N	422N0629	7934	2274	38.8	71	3.9	71	71
42110182 (H7)	-2.9 525 Ovary T	42110182 (H7)	CT4 Bone Marrow	422H0619	480	1375	3.5	80	3.0	80	80
42110182 (H7)	+2.8 261A Ovary T	42110182 (H7)	S10 Skeletal muscle	42230621	8993	3245	34.6	69	5.1	69	69
42110182 (H7)	+2.5 5115 Ovary T (met)	42110182 (H7)	CT10 Small intestine	422C0604	1864	738	8.1	67	2.2	67	67
42110182 (H7)	+2.3 935A Ovary T (SCII)	42110182 (H7)	T2 Skin N	422R0601	2552	1113	12.7	41	2.6	41	41
42110182 (H7)	-2.3 522 Ovary T	42110182 (H7)	CT9 Kidney N	42290627	386	889	3.2	69	3.4	69	69
42110182 (H7)	+2.2 384A Ovary T (met)	42110182 (H7)	272A Dendritic cell	42240608	3516	1567	18.7	55	2.2	55	55
42110182 (H7)	-2.2 382A Ovary T	42110182 (H7)	CT19 Brain N	422Q0610	608	1520	4.2	60	2.3	60	60
42110182 (H7)	+1.9 265A Ovary T	42110182 (H7)	CT5 Heart N	422G0624	2063	1080	13.6	87	3.5	87	87
42110182 (H7)	+1.8 266A Ovary T	42110182 (H7)	S27 Ovary N	42250603	1550	847	7.0	58	2.1	58	58
42110182 (H7)	+1.5 262A Ovary T	42110182 (H7)	334A Large Intestine	422A0622	2559	1651	13.2	73	3.2	73	73
42110182 (H7)	-1.4 386A Ovary T	42110182 (H7)	S40 PBMC (activated)	422J0605	534	738	3.9	62	2.2	62	62
42110182 (H7)	-1.3 288A Ovary T	42110182 (H7)	CT12 Lung N	422V0625	893	1120	5.3	66	3.1	66	66
42110182 (H7)	-1.3 335A Ovary T	42110182 (H7)	S7 Ovary N	42220626	440	567	3.3	60	2.2	60	60
42110182 (H7)	+1.2 9485 OT 1-P (SCID)	42110182 (H7)	9485 OT 5-P (SCID)	422Y0602	4188	3529	21.6	66	9.5	66	66
42110182 (H7)	+1.1 428A Ovary T (met)	42110182 (H7)	243A Esophagus N	42240612	725	689	6.2	65	2.8	65	65
42110182 (H7)	-1.0 201A Ovary T	42110182 (H7)	S6 Stomach N	422W0620	1008	1018	7.4	62	3.2	62	62

Fig. 12

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Gene Name	Ref. Probe 1	P1	P2 Name	Probe 2	QXID	Probe1 Value	Probe2 Value	Probe1 S/B	Probe2 S/B
421V0189 (D1)	+33.2 426A Ovary T (met)	421V0189 (D1)	415A Aorta N	422X0611	8072	243	55.2	67	2.4
421V0189 (D1)	+13.7 523 Ovary T	421V0189 (D1)	S36 Spinal Cord N	422G0628	7367	537	42.6	69	2.5
421V0189 (D1)	+12.6 429A Ovary T (met)	421V0189 (D1)	344A Ovary N	422H0614	2850	227	21.7	64	3.5
421V0189 (D1)	+8.0 383A Ovary T	421V0189 (D1)	S91 Fetal tissue	422X0607	11711	1469	54.0	58	2.2
421V0189 (D1)	+7.3 263A Ovary T	421V0189 (D1)	S73 Breast N	422H0623	6909	952	37.8	69	2.6
421V0189 (D1)	+5.8 525 Ovary T	421V0189 (D1)	CT4 Bone Marrow	422H0619	208	1210	2.1	44	2.9
421V0189 (D1)	+5.0 205A Ovary T	421V0189 (D1)	270A Liver N	422Q0605	8676	1737	52.3	57	2.6
421V0189 (D1)	+4.5 383A Ovary T (met)	421V0189 (D1)	I1 Colon N	422B0609	3149	707	17.4	57	2.0
421V0189 (D1)	+4.4 261A Ovary T	421V0189 (D1)	S10 Skeletal muscle	422J0621	6332	1443	29.1	77	2.9
421V0189 (D1)	+4.2 264A Ovary T	421V0189 (D1)	S2 Pancreas N	422N0629	7612	1809	38.1	79	3.3
421V0189 (D1)	+3.2 382A Ovary T	421V0189 (D1)	CT19 Brain N	422Q0610	468	1508	3.4	60	2.3
421V0189 (D1)	+2.9 933A Ovary T (SCII)	421V0189 (D1)	I2 Skin N	422R0601	2300	860	12.3	51	2.1
421V0189 (D1)	+2.5 5115 Ovary T (met)	421V0189 (D1)	CT10 Small intestine	422C0604	1424	569	6.7	61	2.1
421V0189 (D1)	+2.4 265A Ovary T	421V0189 (D1)	CT5 Heart N	422O0624	1742	723	11.8	70	2.8
421V0189 (D1)	+2.3 384A Ovary T (met)	421V0189 (D1)	272A Dendritic cell	422A0608	3083	1342	17.0	62	2.0
421V0189 (D1)	+1.9 266A Ovary T	421V0189 (D1)	S27 Ovary N	42250605	1370	732	8.0	47	2.0
421V0189 (D1)	+1.9 386A Ovary T	421V0189 (D1)	S40 PBMC (activa)	422J0605	307	580	2.6	41	2.0
421V0189 (D1)	+1.7 262A Ovary T	421V0189 (D1)	334A Large Intestine	422A0622	2097	1202	11.2	86	2.7
421V0189 (D1)	+1.3 335A Ovary T	421V0189 (D1)	S7 Ovary N	42220626	373	470	2.9	47	2.0
421V0189 (D1)	+1.1 288A Ovary T	421V0189 (D1)	CT12 Lung N	422V0625	969	1094	5.6	72	2.9
421V0189 (D1)	+1.1 201A Ovary T	421V0189 (D1)	S6 Stomach N	422W0620	750	672	5.6	62	2.4
421V0189 (D1)	+1.1 428A Ovary T (met)	421V0189 (D1)	243A Esophagus	N422A0612	498	446	4.2	73	2.1
421V0189 (D1)	+1.0 9485 OT 1-P (SCID)	421V0189 (D1)	9485 OT 5-P (SCID)	422Y0602	3117	3174	16.7	91	8.2
421V0189 (D1)	S22 Ovary T	421V0189 (D1)	CT9 Kidney N	42290627	224	409	2.3	48	2.3

Fig. 13

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Gene Name	Ref. Probe 1	Probe 2	Probe 1	Probe 2	Probe 1	Probe 2	Probe 1	Probe 2
Gene Name	Exp. Name	P2 Name	Value	Value	S/B	S/B	A*	A*
421H0187 (E11)	+20.2 426A Ovary T (met)	415A Adip N	5441	270	36.3	2.3	50	50
421H0187 (E11)	+10.0 523 Ovary T	556 Spinal Cord N	5318	533	27.1	2.3	56	56
421H0187 (E11)	+8.3 429A Ovary T (met)	364A Ovary N	1252	150	10.1	2.5	58	58
421H0187 (E11)	+5.7 385A Ovary T	591 Fetal tissue	9507	1668	35.8	2.1	45	45
421H0187 (E11)	+4.4 205A Ovary T	270A Liver N	5456	1235	31.1	2.0	50	50
421H0187 (E11)	+4.2 265A Ovary T	CTS Heart N	1834	438	11.9	2.0	48	48
421H0187 (E11)	+4.1 382A Ovary T	CT19 Brain N	309	1259	2.6	2.0	48	48
421H0187 (E11)	+3.6 261A Ovary T	S10 Skeletal muscle	3733	1036	17.7	2.3	55	55
421H0187 (E11)	+3.4 263A Ovary T	S73 Breast N	4163	1239	23.0	3.0	62	62
421H0187 (E11)	+2.5 5115 Ovary T (met)	CT10 Small intestine	1565	627	8.8	2.1	47	47
421H0187 (E11)	+2.1 264A Ovary T	S2 Pancreas N	3455	1630	14.9	3.0	60	60
421H0187 (E11)	+2.1 384A Ovary T (met)	272A Dendritic cell	2667	1270	13.4	1.9	44	44
421H0187 (E11)	+2.1 522 Ovary T	CT9 Kidney N	291	605	2.4	2.5	51	51
421H0187 (E11)	+1.7 366A Ovary T	S40 PBMC (activated)	410	687	3.2	2.0	47	47
421H0187 (E11)	+1.6 934 Ovary T (SCIT)	T2 Skin N	1622	984	7.9	2.2	44	44
421H0187 (E11)	+1.5 262A Ovary T	334A Large Intestine	1892	1245	10.1	2.6	50	50
421H0187 (E11)	+1.4 428A Ovary T (met)	CT12 Lung N	604	908	4.1	2.6	62	62
421H0187 (E11)	+1.3 335A Ovary T	243A Esophagus N	236	325	2.7	1.9	78	78
421H0187 (E11)	+1.2 201A Ovary T	S7 Ovary N	382	501	2.9	2.0	58	58
421H0187 (E11)	+1.0 2485 OT 1-P (SCID)	S6 Spleen N	558	677	4.2	2.3	58	58
421H0187 (E11)		9485 OT 5-P (SCID)	2582	2493	15.1	6.3	57	57
421H0187 (E11)		I1 Colon N	2261	562	12.5	1.7	38	38
421H0187 (E11)		S27 Ovary N	1739	965	9.7	2.2	36	36
421H0187 (E11)		CT4 Bone Marrow	283	845	2.2	2.2	44	44

Fig. 14

35/101

11721-1

ACGGTTTCAATGGACACTTTTATTGTTTACTTAATGGATCATCAATTTTGTCTCACTACCTACAAATGGAATTT
CATCTTGTTCATGCTGAGTAGTGAAACAGTGACAAAGCTAATCATAATAACCTACATCAAAAGAGAACTAAG
CTAACACTGCTCACTTTCTTTTTAACAGGCAAAATATAAATATATGCACTCTAXAATGCACAATGGTTTAGTCA
CTAAAAAATTCAAATGGGATCTTGAAGAATGTATGCAAATCCAGGGTGCAGTGAAGATGAGCTGAGATGCTGTG
CAACTGTTTAAGGGTTCCTGGCACTGCATCTCTGGCCACTAGCTGAATCTTGACATGGAAGGTTTTAGCTAAT
GCCAAGTGGAGATGCAGAAAATGCTAAGTTGACTTAGGGGCTGTGCACAGGAACTAAAAGGCAGGAAAGTACTA
AATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAGCTCCAACTGGCACCACCCCACTGCTG
TCACATGGCTGACTTTATCCTCCGTGTTCCATTTGGCACAGCAAGTGGCAGTG

11721-2

AAGGCTGGTGGGTTTTGATCCTGCTGGAGAACCTCCGCTTTCATGTGGAGGAAGAAGGGAAGGGAAGATGC
TTCTGGGAACAAGGTTAAAGCCGAGCCAGCCAAAATAGAAGCTTTCAGGCTTCACTTTCCAAGCTAGGGGATG
TCTATGTCAATGATGCTTTTGGCACTGCTCACAGAGCCACAGCTCCATGGTAGGAGTCAATCTGCCACAGAAG
GCTGGTGGGTTTTGATGAAGAAGGAGCTGAACACTTTGCAAAGGCCTTGGAGAGCCAGAGCGACCCTTCT
GGCCATCTGGGCGGAGCTAAAGTTGCAGACAAGATCCAGCTCATCAATAATATGCTGGACAAAGTCAATGAGA
TGATTATTGGTGGTGAATGGCTTTTACCTTCTTAAGGTGCTCAACAACATGGAGATTGGCACTTCTCTGTTT
GATGAAGAGGGAGCCAAGATTGTCAAAGACCTAATGTCCAAAGCTGAGAAGAATGGTGTGAAGATTACCTTGCC
TGTTGACTTTGTCACTGCTGACAAGTTTGATGA

11724-1

TTTGTTCCTTACATTTTTCTAAAGAGTTACTTAATCAGTCAACTGGTCTTTGAGACTCTTAAGTTCTGATTCC
AACTTAGCTAATTCATTCTGAGAACTGTGGTATAGGTGGCGTGTCTCTTCTAGCTGGGACAAAAGTTCTTGT
TTCCCCCTGTAGAGTATCACAGACCTTCTGCTGAAGCTGGACCTCTGTCTGGGCCTTGGACTCCCAATCTGCT
TGTCTGTTCAAGCCTGGAAATGTTAATCTTTAATCTTCCATATGGATGGACATCTGTCTAAGTTGATCCTTT
AGAACTGCAATTATCTTCTTTGAGTCTAATTTCTTCTTCTTGTCTTGAATCGCATCACTAACTTCTCTC
CCATTTCTTAGCTTCATCTATCACCTGTGACGATCATCTGGAGGGAAGACATGCTCTTAGTAAAGGCTGCAA
GCTGGGTACAGTACTGTCCAAGTTTTCTGAAGTTGCTGAACCTTCTTGTCTTCTTGTTCAAAGTAACCTGA
ATCTCTCAATTGTCTCTTCCAAGTGGACTTTTTCTCTGCGCAAAGCATCCAG

11724-2

TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTCAATCAATCAAAGGATTCA
GCATGTGGTGAAGCTGTGAGGCAAGAGAAACAAGAACTGTATGGCAAGTTAAGAAGCACAGAGGCAAAACAAGA
AGGAGACAGAAAAGCAGTTGCAGGAAGCTGAGCAAGAAATGGAGGAAATGAAAGAAAAGATGAGAAAGTTTGCT
AAATCTAAACAGCAGAAAATCCTAGAGCTGGAAGAAGAGAATGACCGGCTTAGGGCAGAGGTGCACCTGCAGG
AGATACAGCTAAAGAGTGTATGGAACACTTCTTTCTTCCAATGCCAGCATGAAGGAAGAACTTGAAGGGTCA
AAATGGAGTATGAAACCTTTCTAAGAAGTTTCACTCTTTAATGTCTGAGAAAGACTCTCTAAGTGAAGAGGTT
CAAGATTTAAAGCATCAGATAGAAGGTAATGTATCTAAACAAGCTAACCTAGAGGCCACCGAGAAACATGATAA
CCAACGAATGTCACTGAAGAGGGAACACAGTCTATACCAGGT

Fig. 15A

36/101

11725-32-1.2

AAGCCAATAATCACCATTTATTACTTAATATATGCCAACCCTGTACTTGGCAGTTCACAAATTCTCACCGTTA
CAACAACCCCATGAGGTATTTATTTCCATTCTATAGATAGGGAAACCACAGCTCAAGTAAGTTAGGAACTGAG
CCAAGTATACACAGAATACGAAGTGGCAAACTAGAAGGAAAGACTGACACTGCTATCTGCTGGCCTCCAGTGT
CCTGGCTCTTTTACACGGGtTCAATGTCTCCAGCGCTGCTGCTGCTGCTGCATTACCATGCCCTCATTGTTTT
TCTTCCTCTGGTGTTCAACTGCATCCTTCAAAGAATCTAACTCATTCCAGAGACCACTTATTTCTTTCTCTCTT
TCTGAAATTACTTTTAATAATTCTTCATGAGGGGAAAAGAAGATGCCTGTTGGTAGTTTTGTTGTTAAGCTG
CTCAATTTGGGACTTAAACAATTTGTTTTCATCTTGTACATCCTGTAACAGCTGTGTTTTGCTAGAAAGATCAC
TCTCCCTCTCTTTAGCATGGCTTCAACCTCTTCAATTCATTTTCTTTTCTTTCAACACAATCTCAAGTTCT
TCAAAGTGTGATGCAGAAGAGGCTCTTTCAAGTTATGTTGTGCTACTTCTGAACATGTGCTTTTAAAGATTC
ATTTCTCTCTGAAGATCCTGTAACCACTTCCCTGTATTGGCTAGGTCTTTCTCTTTCTTTCCAAAACAGCCT
TCATGGTATTCATCTGTTCTCTTTCTTTTAAATAAGTTCAGGAGCTTCAGAAC

11726-1&2

CAAGCTTTTTTTTTTTTTTAAAAAGTGTTAGCATTAAATGTTTTATTGTCACGCAGATGGCAACTGGGTTTATG
TCTTCATATTTTATATTTTGTAAATTAATAAATTACAAGTTTTAAATAGCCAATGGCTGGTTATATTTTACAG
AAACATGATTAGACTAATTCATTAATGGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCT
TTTGTCCCTTCTTAAAAAAGTGAATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCA
TCCACATCTACTTCAAGGAATATCACGTTGGAATACTTTTAGAGAGGGAATGAAAGAAAGGCTTGATCATTTT
GCAAGGCCACACACCGTGGCTGAGAAGTCAACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAA
AAGCAGTCTTGCTCTCGATCTGCTTACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGA
AATGGATCCAAAGCACCAACAGAGCTTCAAGACTCGCTGCTTGGCTTGAATTCGGATCCGATATCGCCATGGC
CT

11727-1&2

AAGTGTTAGCATTAAATGTTTTATTGTCACGCAGATGGCAACTGGGTTTATGTTCTTCATATTTTATATTTTGT
AATTAATAAATTMCAAGTTTTAAATAGCCAATGGCTGGTTATATTTTACAGAAAACATGATTAGACTAATTCAT
TAATGGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCTTTTGTCCCTTCTTAAAAAAGTGG
AATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCATCCACATCTACTTCAAGGAATAT
CACGTTGGAATACTTTTACAGAGAGGGAATGAAAGAAAGGCTTGATCATTTTGAAGGCCACACACCGTGGCTG
AGAAGTCAACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAAAAGCAGTCTTGCTCTCGATCTGC
TTCACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGAAATGGATCCAAAGCACCAACAG
AGCTTCAAGACTCGCTGCTTGGCATGAATTCGGATCCGA

Fig. 15B

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11728.1.40.19.19

TACAACTTTATTGAAACGCACACGCGCACACACACAAACACCCCTGTGGATAGGGAAAAGCACCTGGCCACAG
GGTCCACTGAAACGGGGAGGGGATGGCAGCTTGTAAATGTGGCTTTTGCCACAACCCCTTCTGACAGGGAAGGC
CTTAGATTGAGGCCCCACCTCCCATGGTGATGGGGAGCTCAGAATGGGGTCCAGGGAGAATTTGGTTAGGGGGA
GGTGCTAGGGAGGCATGAGCAGAGGGCACCCCTCCGAGTGGGGTCCGAGGGCTGCAGAGTCTTCAGTACTGTCC
CTCACAGCAGCTGTCTCAAGGCTGGGTCCCTCAAAGGGGCGTCCAGCGCGGGGCCTCCCTGCGCAAACACTTG
GTACCCCTGGCTGCGCAGCGGAAGCCAGCAGGACAGCAGTGGCGCGATCAGCACAAACAGACGCCCTGGCGGTA
GGGACAGCAGGCCAGCCCTGTCGGTTGTCTCGGCAGCAGGTCTGGTTATCATGGCAGAAGTGTCTTCCCACA
CTTCACGTCTTCACACCCACGTGAXGGCTACXGGCCAGGAAG

11728.2.40.19.19

CCCGTGGGTGCCATCCACGGAGTTGTTACCTGATCTTTGGAAGCAGGATCGCCCGTCTGCACTGCAGTGGAAGC
CCCGTGGGCAGCAGTGATGGCCATCCCGCATGCCACGGCTCTGGGAAGGGGCAGCAACTGGAAGTCCCTGAG
ACGGTAAAGATGCAGGAGTGGCCGGCAGAGCAGTGGGCATCAACCTGGCAGGGGCCACCCAGATGCCTGCTCAG
TGTTGTGGGCCATTTGTCCAGAAGGGGACGGCAGCAGTGTAGCTGGCTCCTCCGGGGTCCAGGCAGCAGGCCA
CAGGGCAGAACTGACCATCTGGGCACCGCTTCCAGCCACCAGCCCTGCTGTTAAGGCCACCCAGCTCACCAGG
GTCCACATGGTCTGCCTGCGTCCGACTCCGCGGTCTTGGGCCCTGATGGTTCTACCTGCTGTGAGCTGCCAG
TGGGAAGTATGGCTGCTGCCAATGCCAACGCCACCTGCTGCTCCGATCACCTGCACTGCTGCCCCAAGACACT
GTGTGTGACCTGATCCAGAGTAAGTGCCTCTCCAAGGAGAACG

11730-1

GAATCACCTTTCTGGTTTAGCTAGTACTTTGTACAGAACAATGAGGTTTCCACAGCGGAGTCTCCCTGGGCTC
TGTTTGGCTCTCGGTAAGGCAGGCCTACACCTTTTCTCTCTATGGAGAGGGGAATATGCATTAAGGTGAA
AAGTCACCTTCCAAAAGTGAGAAAGGATTGATTGCTGCTTCAGGACTGTGGAATTATTTGGAATGTTTTACA
AATGGTTGCTACAAAACAACAAAAAGGTAATTACAAAATGTGTACATCACAAATGCTTTTTAAAGACATTAT
GCATTGTGCTCACATTCCCTTAAATGTTGTTTCAAAGGTGCTCAGCCTCTAGCCAGCTGGATTCTCCGGGAA
GAGGCAGAGACAGTTTGGCGAAAAAGACACAGGGAAGGAGGGGTGGTGAAGGAGAAAGCAGCCTTCCAGTTA
AAGATCAGCCCTCAGTTAAAGGTCAGCTTCCCGCAXGCTGGCCTCAXGCGGAGTCTGGGTGAGAGGGAGGAGCA
GCAGCAGGGTGGGACTGGGGCGT

11730-2

AACCGGAGCGCAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGAT
CCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGAGAAA
GGCGGGCCCCGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTG
GACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGA
GAGAGGTATGAAGGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAAGATGGAATCCAGGAAATCCAATCA
AAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAA
GGAGACTTGGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGATTAG
ACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

Fig. 15C

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11732.1contig

GAGAACTTGGCCTTTATTGTGGGCCCAGGAGGGCACAAAGGTCAGGAGGCCCAAGGGAGGGATCTGGTTTTCTG
GATAGCCAGGTCATAGCATGGGTATCAGTAGGAATCCGCTGTAGCTGCACAGGCCTCACTTGCTGCAGTTCGGG
GGAGAACACCTGCACTGCATGGCGTTGATGACCTCGTGGTACACGACAGGCCATTGGTGCAGTGCAAGGGCAC
GCGCATGGGCTCCGTCTCGAGGGCAGGCAGCAGGAGCATTGCTCCTGCACATCCTCGATGTCAATGGAGTACA
CAGCTTTGCTGGCACACTTTCCCTGGCAGTAATGAATGTCCACTTCCTCTTGGGACTTACAATCTCCCACTTTG
ATGTACTGCACCTTGGCTGTGATGTCTTTGCAATCAGGCTCCTCACATGTGTACAGCAGGTGCCTGGAATTTT
CACGATTTTGCCTCCTTCAGCCAGACACTTGTGTTTCATCAATGGTGGGCAGCCCGTGACCCTCTTCTCCAGA
TGTA CTCTCTCT

11732.2contig

GCCTGGACCTTGCCGGATCAGTGCCACACAGTGACTTGCTTGGCAAATGGCCAGACCTTGCTGCAGAGTCATCG
TGTC AATTGTGACCATGGACCCCGCCTTCATGTGCCAACAGCCAGTCTCCTGTTCCGGGTGGAGGAGACGTGTG
GCTGCCGCTGGACCTGCCCTTGTGTGTGCACGGGCAGTTCCTCGGCACATCGTCACCTTCGATGGGCAGAAT
TTCAAGCTTACTGGTAGCTGCTCCTATGTCATCTTTCAAACAAGGAGCAGGACCTGGAAGTGCTCCTCCACAA
TGGGGCTGCAGCCCCGGGGCAAACAAGCCTGCATGAAGTCCATTGAGATTAAGCATGCTGGCGTCTCTGCTG
AGCTGCACAGTAACATGGAGATGGCAGTGGATGGGAGACTGGTCCTTGCCCGTACGTTGGTGAAACATGGAA
GTCAGCATCTACGGCGCTATCATGTATGAAGTCAGGTTTACCCATCTTGGCCACATCCTCACATACACCGCCXC
AAAACAACGAGTT

11735-1-2

AGATCAACCTCTGCTGGTCAGGAGGAATGCCTTCCTTGCTTGGATCTTTGCTTTGACGTTCTCGATAGTRWCA
aCTKKRYTSRAMSKMAAGKGYRATGRWMTTKSYWGRASYKTMWWMRSGRARAYTTaGaCAYCCCMCCTCWgAG
aCGSAGKACCARGTGCAgAgGTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGTCCATCTTCCAGCTGT
TTCCCAGCAAAGATCAACCTCTGCTGATCAGGAGGGATGCCTTCCTTATCTTGGATCTTTGCCTTGACATTCTC
GATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATYTGATCCAC
CTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGYCCATCTTCC
AGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCCTTGTCYTGGATCTTTGCTTTGA
CRTTCTCRATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATCTGC
ATCCCACCTCTAA

11740.2.contig

AAGTCACAAACAGACAAAGATTATTACCAGCTGCAAGCTATATTAGAAGCTGAACGAAGAGACAGAGGTCATGA
TTCTGAGATGATTGGAGACCTTCAAGCTCGAATTACATCTTTACAAGAGGAGGTGAAGCATCTCAAACATAATC
TCGAAAAAGTGGAAGGAGAAAGAAAAGAGGCTCAAGACATGCTTAATCACTCAGAAAAGGAAAAGAATAATTTA
GAGATAGATTTAACTACAACTTAAATCATTACAACAACGGTTAGAACAAGAGGTAAATGAACACAAAGTAAC
CAAAGCTCGTTTAACTGACAAACATCAATCTATTGAAGAGGCAAGTCTGTGGCAATGTGTGAGATGGAAAAA
AGCTGAAAGAAGAAAGAGAAGCTCGAGAGAAGGCTGAAAATCGGGTTGTTGAGATTGAGAAACAGTGTTCCATG
CTAGACGTTGATCTGAAGCAATCTCAGCAGAACTAGAACATTTGACTGGAAATAAGAAAGGATGGAGGATGA
AGTTAAGAATCTA

Fig. 15D

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11765.2&64.2.contig

CGCCTCCACCATGTCCATCAGGGTGACCCAGAAGTCCTACAAGGTGTCCACCTCTGGCCCCGGGCTTCAGCA
GCCGCTCCTACACGAGTGGGCCCCGGTTCGCCATCAGCTCCTCGAGCTTCTCCGAGTGGGCAGCAGCAACTTT
CGCGGTGGCCTGGGCGGCGGCTATGGTGGGGCCAGCGGCATGGGAGGCATCACCGCAGTTACGGTCAACCAGAG
CCTGCTGAGCCCCCTTGCTCCTGGAGGTGGACCCCAACATCCAGGCCGTGCGCACCCAGGAGAAGGAGCAGATCA
AGACCCCTCAACAACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCTGGAGCAGCAGAACAAGATGCTGGAG
ACCAAGTGGAGCCTCCTGCAGCAGCAGAAGACGGCTCGAAGCAACATGGACAACATGTTTCGAGAGCTACATCAA
CARCCTTAGGCGGCAGCTGGAGACTCTGGGCCAGGAGAAGCTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGG
GGCTGGTGGAGGACTTCAAGAACAAGTATGAGGATGAGATCAATAAGCGTACAGAGATGGAGAACGAATTTGTC
CTCATCAAGAAGGATGTGGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACCGA
CGAGATCAACTTCCTCAGGCAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCAGATCTCGGACACATCTG
TGGTGTCTGCATGGACAACAGCCGCTCCCTGGACATGGACAGCATCATTGCTGAGGTCAAGGCACAGTACGAG
GATATTGCCAACCGCAGCCGGGCTGAGGCTGAGAGCATGTACCAGGTCAAGTATGAGGAGCTGCAGAGCCTGGC
TGGGAAGCACGGGGATGACCTGCGGCGCACAAAGACTGAGATCTCTGAGATGAACCCGGAACATCAGCCCGGCT
XCAGGCTGAGATTGAGGGCTCAAAGGCCAGAXGGCTTTCCTGGAXGXCCGCCAT

11767.2.contig

CCCGGAGCCAGCCAACGAGCGGAAAATGGCAGACAATTTTTCGCTCCATGATGCGTTATCTGGGTCTGGAAACC
CAAACCTCAAGGATGGCCTGGCGCATGGGGGAACCAGCCTGCTGGGGCAGGGGGCTACCCAGGGGCTTCCTAT
CCTGGGGCTACCCCGGGCAGGCACCCCAAGGGCTTATCCTGGACAGGCACCTCCAGGCGCCTACCTGGAGC
ACCTGGAGCTTATCCCGGAGCACCTGCACCTGGAGTCTACCCAGGGCCACCCAGCGGCCCTGGGGCTACCCAT
CTTCTGGACAGCCAAGTGCCACCGGAGCCTACCTGCCACTGGCCCCTATGGCGCCCCTGCTGGGCCACTGATT
GTGCCTTATAACCTGCCTTTGCCTGGGGGAGTGGTGCCTCGCATGCTGATAACAATTCTGGGCACGGTGAAGCC
CAATGCAAACAGAATTGCTTTAGATTTCAAAGAGGGAATGATGTTGCCTTCCACTTTAACCACGCTTCAATG
AGAACAACAGGAGAGTCATTGGTTGCAATACAAAGCTGGATAA

11768-1&2

GGGAATGCAACAACTTTATTGAAAGGAAAGTGAATGAAATTTGTTGAAACCTTAAAAGGGGAAACTTAGACAC
CCCCCTCRAGCGMAGKACCARGTGCARAgTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTRCGWCCATC
TTCCAGCTGTTTTYCCRGCAAAGATCAACCTCTGCTGATCAGGAGGRATGCCCTTCTTATCTTGGATCTTTGCCT
TGACATTCTCGATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATY
TGCATCCACCTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCG
YCCATCTTCCAGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCTTGTCTGTGGATC
TTTGCTTACRTTCTCAATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCAC
GAAGATCTGCATCCACCTCTAAGACGGAGCACCAGGTGCAGGGTGGACTCTTTCTGGATGgTTGTAGTCAGAC
AGGGTGCGTCCATCTTCCAGCTGTTTCCAGCAAAGATCAACCT

Fig. 15E

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11768-1&2-11735-1&2

AGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACCATCCAGAAAGAGTCCA
CCCTGCACCTGGTGCTCCGTCTTAGAGGTGGGATGCAGATCTTCGTGAAGACCCTGACTGGTAAGACCATCACT
CTCGAAGTGGAGCCGAGTGACACCATTGAGAAYGTCAARGCAAAGATCCARGACAAGGAAGGCATYCCCTCTGA
CCAGCAGAGGTTGATCTTTGCTSGGAAAGCAGCTGGAAGATGGRCGCACCCTGTCTGACTACAACATCCAGAAA
GAGTCYACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGATGCRATCTTCGTGAAGACCCTGACTGGTAAGAC
CATCACCCCTCGAGGTGGAGCCCAGTGACACCATCGAGAATGTCAAGGCAAAGATCCAAGATAAGGAAGGCATCC
CTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATC
CAGAAAGAGTCCACcTYTGCACYTGGTMCTBCGtCTYaGAGGKGGGRTGcaaTCTWMGTKWagaCaCtCaCTK
KYAAGRYYaTCAMCMWtgAKKTCgAKYSCASTKWCaCTWTCRAKAAMGTYRWGCAWagaTCCMAGACAAGGAA
GGCATTCTCCTGACCAGCAGAGGTTGATCT

11769.1.contig

ATGGAGTCTCACTCTGTGCGACCAGGCTGGAGCGCTGTGGTGCGATATCGGCTCACTGCAGTCTCCACTTCCTGG
GTTCAAGCGATCCTCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCAGGCGTCACCATAATTTTTGTATT
TTTAGTAGAGACATGGTTTCGCCATGTTGGCTGGGCTGGTCTCGAACTCCTGACCTCAAGTGATCTGTCTGGC
CTCCCAAAGTGTTGGGATTACAGGCGAAAGCCAACGCTCCCGGCCAGGGAACAACCTTTAGAATGAAGGAAATAT
GCAAAAGAACATCACATCAAGGATCAATTAATTACCATCTATTAATTACTATATGTGGGTAATTATGACTATTT
CCCAAGCATTCTACGTTGACTGCTTGAGAAGATGTTTGTCTGCATGGTGGAGAGTGGAGAAGGGCCAGGATTC
TTAGGTT

11769.2.contig

AGCGCGGTCTTCCGGCGCGAGAAAGCTGAAGGTGATGTGGCCGCCCTCAACCGACGCATCCAGCTCGTTGAGGA
GGAGTTGGACAGGGCTCAGGAACGACTGGCCACGGCCCTGCAGAACTGGAGGAGGCAGAAAAAGCTGCAGATG
AGAGTGAGAGAGGAATGAAGGTGATAGAAAACCGGGCCATGAAGGATGAGGAGAAGATGGAGATTCAGGAGATG
CAGCTCAAAGAGGCCAAGCACATTGCGGAAGAGGCTGACCGCAAATACGAGGAGGTAGCTCGTAAGCTGGTCAT
CCTGGAGGGTGAGCTGGAGAGGGCAGAGGAGCGTGCGGAGGTGTCTGAACTAAATGTGGTGACCTGGAAGAAG
AACTCAAGAATGTTACTAACAATCTGAAATCTCTGGAGGCTGCATCTGAAAAGTATTCTGAAAAGGAGGACAAA
TATGAAGAAGAAATTAACCTTCTGTCTGACAACTGAAAGAGGCTGAGACCCGTGCTGAATTTGCAGAGAGAAC
GGTTGCAAACTGGAAAAGACAATTGATGACCTGGAAGAGAACTTGCCACG

11770.1.contig

GTGCACAGGTCCCATTTATTGTAGAAAATAATAATAATTACAGTGATGAATAGCTCTTCTTAAATTACAAAACA
GAAACCACAAAGAAGGAAGAGGAAAAACCCAGGACTTCCAAGGGTGAAGCTGTCCCCTCCTCCCTGCCACCCT
CCCAGGCTCATTAGTGTCTTGAAGGGGCAGAGGACTCAGAGGGGATCAGTCTCCAGGGGCCCTGGGCTGAAG
CGGGTGAGGCAGAGAGTCTGAGGCCACAGAGCTGGGCAACCTGAGCCGCCTCTCTGGCCCCCTCCCCACCAC
TGCCCAAACCTGTTTACAGCACCTTCGCCCTCCCCTCTAAACCCGTCCATCCACTCTGCACCTCCCAGGCAGG
TGGGTGGGCCAGGCCTCAGCCATACTCCTGGGCGCGGGTTTCGGTGAGCAAGGCACAGTCCAGAGGTGATATC
AAGGCCT

Fig. 15F

41/101

11770.2.contig

GCAAGGAAGTGGTCTGCTCACACTTGCTGGCTTGCGCATCAGGACTGGCTTTATCTCCTGACTCACGGTGCAAA
GGTGCACCTCTGCGAACGTTAAGTCCGTCCCCAGCGCTTGGAACTCTACGGCCCCACAGCCGGATCCCCTCAGC
CTTCCAGGTCTCAACTCCCGTGGACGCTGAACAATGGCCTCCATGGGGCTACAGGTAATGGGCATCGCGCTGG
CCGTCTGGGCTGGCTGGCCGTCATGCTGTGCTGCGCGCTGCCCATGTGGCGCGTGACGGCCTTCATCGGCAGC
AACATTGTCACCTCGCAGACCATCTGGGAGGGCCTATGGATGAACTGCGTGGTGCAGAGCACCGGCCAGATGCA
GTGCAAGGTGTACGACTCGCTGCTGGCACTGCCGACGACCTGCAGGCGGCCCGGCCCTCGTCATCATCA

11773.1.contig

TGCAAAAGGGACACAGGGGTTCAAAAATAAAAATTTCTTCCCCCTCCCCAACCTGTACCCAGCTCCCCGA
CCACAACCCCTTCTCCCCGGGAAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAGGCC
GGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCAAATATAAATACXTGTGTCAGAACTGGAAAATCCTCCAGC
ACCCACCACCAAGCACTCTCGTTTTCTGCCGGTGTGGAGAGGGGCGGGGGCAGGGGCGCCAGGCACCGG
CTGGCTGCGGTCTACTGCATCCGCTGGGTGTGCACCCGCGAGCCTCCTGCTGCTCATTGTAGAAGAGATGACA
CTCGGGGTCCCCCGGATGGTGGGGGCTCCCTGGATCAGTTCCCGGTGTTGGGGTTCACACACCAGCACTCCC
CACGCTGCCCCGTTCAAGAGACATCTTGCACTGTTTGAGGTTGTACAGGCCATGCTTGTCACAGTTG

11778.1.contig

GGGTTGGAGGGACTGGTCTTTATTTCAAAAAGACACTTGTCATATTCAGTATCAAAACAGTTGCACTATTGA
TTTCTCTTTCTCCAATCGGCCCAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGA
TGTACACCTAACAGACCTCCTAGAAACCTTACCAGAAAATGGGGACTGGGTAGGGAAGGAACTTAAAGATCA
ACAACTGCCAGCCACGGACTGCAGAGGCTGTACAGCCAGATGGGTGGCCAGGGTGCCACAAACCCAAAGC
AAAGTTTCAAAATAATATAAAATTTAAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGAT
ACAAAGCACAAATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAGTTTCA
CATGGCTAAATCAGTGGCAAAAACACAGTCTTCTTTCTTTCTTTCAAGGAGGCAGGAAAGCAATTAAGTG
GTCACCTCAACATAAGGGGGACATGATCCATTCTGTAAGCAGTTGTGAAGGGG

11778-2&30-2

CAGGAACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCA
AGATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCTCCAGCGAGAAGTTGAGGGA
GAAAGGCGGGCCCGGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGA
GCTGGACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGA
GTGAGAGAGGTATGAAGGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAAGATGGAACCTCAGGAAATCCAA
CTCAAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCAT
TGAAGGAGACTTGGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGA
TTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

Fig. 15G

42/101

11782.1.contig

ATCTACGTCATCAATCAGGCTGGAGACACCATGTTCAATCGAGCTAAGCTGCTCAATATTGGCTTTCAAGAGGC
CTTGAAGGACTATGATTACAACCTGCTTTGTGTTGAGTGATGTGGACCTCATTCCGATGGACGACCGTAATGCCT
ACAGGTGTTTTTCGCAGCCACGGCACATTTCTGTTGCAATGGACAAGTTCGGGTTTAGCCTGCCATATGTTGAG
TATTTTGGAGGTGTCTCTGCTCTCAGTAAACAACAGTTTCTTGCCATCAATGGATTCCCTAATAATTATTGGGG
TTGGGGAGGAGAAGATGACGACATTTTAAACAGATTAGTTCATAAAGGCATGTCTATATCACGTCCAAATGCTG
TAGTAGGGAGGTGTCGAATGATCCGGCATTCAAGAGACAAGAAAAATGAGCCCAATCCTCAGAGGTTTGACCGG
ATCGCACATACAAAGGAAACGATGCGCTTCGATGGTTTGAACCTACTTACCTACAAGGTGTTGGATGTCAGAGA
TACCCGTTATATACCCAAATCAC

11782.2.contig

CTAGACCTCTAATTAAAAGGCACAATCATGCTGGAGAATGAACAGTCTGACCCCGAGGGCCACAGCGAATTTTA
GGGAAGGAGGCAAAGAGGTGAGAAGGGAAAGGAAAGAAGGAAGGAGAACAATAAGAAGTGGAGACGTTGG
GTGGGTGAGGGAGTGTGGTGGAGGCTCGGAGAGATGGTAAACAAACCTGACTGCTATGAGTTTTCAACCCATA
GTCTAGGGCCATGAGGGCGTCAGTTCTTGGTGGCTGAGGGTCTTCCACCCAGCCACCTGGGGGAGTGGAGTG
GGGAGTTCTGCCAGGTAAGCAGATGTTGTCTCCCAAGTTCCTGACCCAGATGTCTGGCAGGATAACGCTGACCT
GTTCCCTCAACAAGGGACCTGAAAGTAATTTTGCTCTTTAC

11783-1 & 2

CCGAATTC AAGCGTCAACGATCCYTCCCTTACCATCAAATCAATTGGCCACCAATGGTACTGAACCTACGAGTA
CACCGACTACGGGCGGACTAATCTTCAACTCCTACATACTTCCCCATTATTCCTAGAACCAGGCGACCTGCGA
CTCCTTGACGTTGACAATCGAGTAGTACTCCCGATTGAAGCCCCATTTCGTATAATAATTACATCACAAGACGT
CTTGCACTCATGAGCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAGCCAAACCACTT
TCACCGCTACACGACCGGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAACCACAGTTTCATGCC
ATCGTCCTAGAATTAATTCCTTAAAAATCTTTGAAATAGGGCCCGTATTTACCCTATAGCACCCCTCTACCC
CCTCTAG

11786.1.contig

GCTCTTCACACTTTTATTGTTAATTCTCTTCACATGGCAGATACAGAGCTGTCGTCTTGAAGACCACCACTGAC
CAGGAAATGCCACTTTTACAAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAGCGT
TGAAGGGTGACCAGCACATTTGCACATGCAAAAAAGGAGTGACCCCAAGGCCTCAACCACACTTCCAGAGCTC
ACCATGGGCTGCAGGTGACTTGCCAGGTTTGGGGTTCGTGAGCTTTCTTGCTGCTGCGGTGGGGAGGCCCTCA
AGAAGTGAAGAGGCCGGGTATGCTTCATGAGTGTTAACATTTACGGGACAAAAGCGCATCATTAGGATAAGGAA
CAGCCACAGCACTTCATGCTTGAGGGTTAGCTGTAGGAGCGGGTGAAAGGATTCAGTTTATGAAAATTTAA
AGCAAACAACGGTTTTTATGCTGGGTGGGAAACAGGAAAACGTGATGTCGGCCAATGACCACCATTTTTCTGCC
CATGTGAAGGTCCCATGAAACC

Fig. 15H

43/101

11786.2.contig

CAAGCGCTTGGCGTTTGGACCCAGTTCAGTGAGGTTCTTGGGTTTTGTGCCTTTGGGGATTTTGGTTTGACCCA
GGGGTCAGCCTTAGGAAGGTCTTCAGGAGGAGGCCGAGTTCCTTCAGTACCACCCCTCTCTCCCACTTTCC
CTCTCCCGGCAACATCTCTGGAATCAACAGCATATTGACACGTTGGAGCCGAGCCTGAACATGCCCCCTGGCC
CCAGCACATGGAAAACCCCTTCCTTGCTAAGGTGTCTGAGTTTCTGGCTCTTGAGGCATTTCCAGACTTGAA
ATTCTCATCAGTCCATTGCTCTTGAGTCTTTCAGAGAACCTCAGATCAGGTGCACCTGGGAGAAAGACTTTGT
CCCCACTTACAGATCTATCTCCTCCCTTGGGAAGGGCAGGAATGGGGACGGTGTATGGAGGGGAAGGGATCTC
CTGCGCCCTTCATTGCCACACTTGGTGGGACCATGAACATCTTAGTGTCTGAGCTTCTCAAATTACTGCAATA
GGA

13691.1&2

AGCGTCAAATCAGAATGGAAAAGACTCAAAACCATCATCAACACCAAGATCAAAAGGACAAGRATCCTTCAAGA
AACAGGAAAAAACTCCTAAAACACCAAAAGGACCTAGTTCTGTAGAAGACATTAAGCAAAAATGCAAGCAAGT
ATAGAAAAAGGTGGTTCTCTTCCCAAAGTGGAAGCCAAATTCATCAATTATGTGAAGAATTGCTTCCGGATGAC
TGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTTAAGAAAATAGTTTAAACAATTTGTTAA
AAAATTTCCGTCTTATTTTCTTTCTGTAACAGTTGATATCTGGCTGTCTTTTTATAATGCAGAGTGAGAACT
TTCCCTACCGTGTGTTGATAAATGTTGTCCAGGTTCTATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTAGTT
TTTAAAGATGGAACTCCACCCCTTGCTTGTTTTAAGTATGTATGGAATGTTATGATAGGACATAGTAGTAGCG
GTGGTCAGACATGGAAATGGTGGGSMGACAAAATATACATGTGAAATAA

13692.1&2

TCCGAATCCAAGCGAATTATGGACAAACGATTCTTTTTAGAGGATTACTTTTTTCAATTTTCGGTTTTAGTAAT
CTAGGCTTTGCCTGTAAAGAATACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATTC
TAGAACCTTTGTATATTTGATAGTATTTCTAACTTTTCACTTTTACTGTTTGCAGTTAATGTTTATGTTCTGC
TATGCAATCGTTTATATGCACGTTTCTTTAATTTTTTAGATTTTCTGGATGTATAGTTTAAACAACAAAAAG
TCTATTTAAACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAAACTTTGTATTTTCT
TTCTTATAGAGGCTTCTAAAAAGGTATTTTATATGTTCTTTTTAACAAATATTGTGTACAACCTTTAAACAT
CAATGTTTGGATCAAAACAAGACCCAGCTTATTTTCTGC

13693.2

TGTGGTGGCGCGGGCTGAGGTGGAGGCCAGGACTCTGACCCTGCCCTGCCTTCAGCAAGGCCCGGCGAGCG
CCGGCCACTACGAACTGCCGTGGGTGAAAAATATAGGCCAGTAAAGCTGAATGAAATTGTGCGGAATGAAGAC
ACCGTGAGCAGGCTAGAGGTCTTTGCAAGGGAAGGAAATGTGCCAACATCATCATTGCGGGCCCTCCAGGAAC
CGGCAAGACCACAAGCATTCTGTGCTTGGCCCGGGCCCTGCTGGGCCAGCACTCAAAGATGCCATGTTGGAAC
TCAATGCTTCAAATGACAGGGGCATTGACGTTGTGAGGAATAAAATTAATGTTTGTCAACAAAAAGTCACT
CTTCCCAAAGGCCGACATAAGATCATCATTCTGGATGAAGCAGACAGCATGACCGACGGAGCCAGCAAGCCTT
GAGGAGAACCATGGAAATCTACTCTAAAACCACTCGTTGCGCCTTGCTTGTAAATGCTTCGGATAAGATCATCGA
GCC

Fig. 15I

44/101

13696.1-13744.1

CTTTGCAAAGCTTTTATTTTCATGTCTGCGGCATGGAATCCACCTGCACATGGCATCTTAGCTGTGAAGGAGAAA
GCAGTGCACGAGAAGGAATGAGTGGGCGGAACCAACGGCCTCCACAAGCTGCCTTCCAGCAGCCTGCCAAGGCC
ATGGCAGAGAGAGACTGCAAACAAACACAAGCAAACAGAGTCTCTTCACAGCTGGAGTCTGAAAGCTCATAGTG
GCATGTGTGAATCTGACAAAATTTAAAGTGTGCATAGTCCATTACATGCATAAAACACTAATAATAATCCTGTT
TACACGTGACTGCAGCAGGCAGGTCCAGCTCCACCACTGCCCTCCTGCCACATCACATCAAGTGCCATGGTTTA
GAGGGTTTTTCATATGTAATTCTTTTATTCTGTAAAAGGTAACAAAATATACAGAACAAAACCTTCCCTTTTTTA
AACTAATGTTACAAATCTGTATTATCACTTGGATATAAATAGTATATAAGCTGATC

13700.1

CAAGGGATATATGTTGAGGGTACRGRGTGACACTGAACAGATCACAAAGCACGAGAAACATTAGTTCTCTCCCT
CCCCAGCGTCTCCTTCGTCTCCCTGGTTTTCCGATGTCCACAGAGTGAGATTGTCCCTAAGTAAGTGCATGATC
AGAGTGCTGKCTTTATAAGACTCTTCATTAGCGTATCCAATTCAGCAATTGCTTCATCAAATGCCGTTTTTGC
CAGGCTACAGGCCTTTTCAGGAGAGTTTGAATCTCATAGTAAAAGACTGAGAAATTTAGTGCCAGACCAAGAC
GAATTGGGTGTGTAGGCTGCATTNCTTTCTTACTAATTTCAAATGCTTCCTGGTAAGCCTGCTGGGAGTTCGAC
ACAAGTGTTTTGTTGTTGCTCCAGATGCCACTTCAGAAAGATACCTAAAATAATCTCCTTTTCATTTTCAAAGT
AGAACAC

13700.2

TCCGGAGCCGGGGTAGTCGCCGCCGCCGCCGCCGGTGCAGCCACTGCAGGCACCGCTGCCGCCGCCTGAGTAGT
GGGCTTAGGAAGGAAGAGGTCTCTCGCTCGGAGCTTCGCTCGGAAGGGTCTTTGTTCCCTGCAGCCCTCCCAC
GGGAATGACAATGGATAAAAGTGAGCTGGTACAGAAAGCCAAACTCGCTGAGCAGGCTGAGCGATATGATGATA
TGGCTGCAGCCATGAAGGCAGTACAGAACAGGGGCATGAACTCTCCAACGAAGAGAGAAATCTGCTCTCTGTT
GCCTACAAGAATGTGGTAAGGCCGCCGCCGCTCTTCTGGCGTGTCTCTCCAGCATTGAGCAGAAAACAGAG
AGGAATGAGAAGAAGCAGCAGATGGGCAAAGGTACCGTGAGAAGATAGAGGCAGAACTGCAGGACATCTGCAA
TGATGTTCTGGAGCTTGTTGGACAAATATCTTATTCGAATGCTACACAACCCAGAAA

13701.1

AAAAAGCAGCARGTTCAACACAAAATAGAAATCTCAAATGTAGGATAGAACAAAACCAAGTGTGTGAGGGGGGA
AGCAACAGCAAAAGGAAGAAATGAGATGTTGCAAAAAAGATGGAGGAGGGTCCCTCTCCTCTGGGGACTGAC
TCAAACACTGATGTGGCAGTATACACCATTCCAGAGTCAGGGGTGTTTCTTTTGGGAGTAAGAAAAGGT
GGGGATTAAGAAGACGTTTCTGGAGGCTTAGGGACCAAGGCTGGTCTCTTCCCCCTCCCAACCCCTTGATC
CCTTTCTCTGATCAGGGGAAAGGAGCTCGAATGAGGGAGGTAGAGTTGGAAAGGGAAAGGATTCCACTTGACAG
AATGGGACAGACTCCTTCCCA

Fig. 15J

45/101

13701.2

TGGCAATAGCACAGCCATCCAGGAGCTCTTCARGCGCATCTCGGAGCAGTTCACTGCCATGTTCCGCCGGAAGG
CCTTCCTCCACTGGTACACAGGCGAGGGCATGGACGAGATGGAGTTCACCGAGGCTGAGAGCAACATGAACGAC
CTCGTCTCTGAGTATCAAGCAGTACCAGGATGCCACCGCAGAAGAGGAGGAGGATTTCCGGTGAGGAGGCCGAAG
AGGAGGCCCTAAGGCAGAGCCCCATCACCTCAGGCTTCTCAGTTCCTTAGCCGTCTTACTCAACTGCCCCTTT
CCTCTCCCTCAGAATTTGTGTTTGCTGCCTCTATCTGTTTTTTGTTTTTCTTCTGGGGGGGTCTAGAACAGT
GCCTGGCACATAGTAGGCGCTCAATAAATACTTGGTTGNTGAATGTCTCCT

13702.2

AGCTGGCGCTAGGGCTCGGTTGTGAAATACAGCGTRGTCAGCCCTTGCGCTCAGTGTAGAAACCCACGCCTGTA
AGGTCGGTCTTCGTCCATCTGCTTTTTCTGAAATACCTAAGAGCAGCCACAAAACCTGAACCTCAAGGAAAC
CATAAAGCTTGGAGTGCCTTAATTTTAAACCAGTTTCCAATAAAACGGTTTACTACCT

13704.2-13740.2

GGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCARGCGGCAGCTGAAGATGATGAGGATGACGATGTCTGA
TACCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAAGGAAAAGTTAAA

13706.1

GATGAAAATTAATACTTAAATTAATCAAAAGGCACTACGATACCACCTAAACCTACTGCCTCAGTGGCAGTA
KGCTAAKGAAGATCAAGCTACAGSACATYATCTAATATGAATGTTAGCAATTACATAKARGAAGCATGTTTGC
TTTCCAGAAGACTATGGNACAATGGTCATTWGGGCCCAAGAGGATATTTGGCCNGGAAAGGATCAAGATAGATN
AANGTAAAG

13706.2

GAGTAGCAACGCAAAGCGCTTGGTATTGAGTCTGTGGGSGACTTCGGTTCCGGTCTCTGCAGCAGCCGTGATCG
CTTAGTGGAGTGCTTAGGGTAGTTGGCCAGGATGCCGAATATCAAAATCTTCAGCAGGCAGCTCCCACCAGGAC
TTATCTCASAAAATTGCTGACCGCCTGGGCTGGAGCTAGGCAAGGTGGTGACTAAGAAATTGAGCAACCAGGA
GACCTGTGTGGAAATTGGTGAAAGTGACCGTGGAGAGGATGTCTACATTGTTGAGAGTGGNTGTGGCGAAATC
AATGACAATTTAATGGAGCTTTTGATCATGATTAATGCCTGCAAGATTGCTTCAGCCAGCCGGGTTACTGCAGT
CATCCCATGCTTCCCTTATGCCCCGGCAGGATAAGAAAGATNAGAGCCGGGCCCAATCTCAGCCAAGCTTGG
TGCAAATATGCTATCTGTAGCAGTGCAGATCATATTATCACCATGGACCTACATGCTTCTCAAATTCANGGCTT
TTT

Fig. 15K

46/101

13707.3

ATGCAAAGGGGACACAGGGGGTTCAAAAATAAAAATTTCTCTTCCCCCTCCCCAAACCTGTACCCCAGCTCCC
CGACCACAACCCCTTCTCCCCGGGGAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAG
GCCGGGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCCAAATATAAATACGTGTGTCAGAACTGGAAAATCCTCC
AGCACCCACCACCAAGCACTCTCCGTTTTCTGCCGGTGTGGAGAGGGGCGGNGGGCAGGGGCGCCAGGCAC
CGGCTGGCTGCCGTCTACTGCATCCGCTGGGTGTGCACCCCGCA

13710.2

AGGTTGGAGAAGGTCATGCAGGTGCAGATTGTCCAGGSKCAGCCACAGGGTCAAGCCCAACAGGCCCAGAGTGG
CACTGGACAGACCATGCAGGTGATGCAGCAGATCATCTAAACACAGGAGAGATCCAGCAGATCCCGGTGCAGC
TGAATGCCGGCCAGCTGCAGTATATCCGCTTAGCCAGCCTGTATCAGGCACTCAAGTTGTGCAGGGACAGATC
CAGACACTTGCCACCAATGCTCAACAGATTACACAGACAGAGGTCCAGCAAGGACAGCAGCAGTTCAAGCCAGT
TCACAAGATGGACAGCAGCTCTACCAGATCCAGCAAGTACCATGCCTGCGGGCCANGACCTCGCCAGCCCATG
TTCATCCAGTCAAGCCAACCAGCCCTTCNACGGGCAGGCCCCCAGGTGACCGGCGACTGAAGGGCCTGAGCTG
GCAAGGCCAANGACACCAACACAATTTTTGCCATACAGCCCCCAGGCAATGGGCACAGCCTTTCTTCCCAGAG
GAC

13710-1

TGAGATTTATTGCATTTTCATGCAGCTTGAAGTCCATGCAAAGGRGACTAGCACAGTTTTTAATGCATTTAAAAA
ATAAAAGGGAGGTGGGCAGCAAACACACAAAGTCTAGTTTCTGGGTCCCTGGGAGAAAAGAGTGTGGCAATG
AATCCACCCACTCTCCACAGGAATAAATCTGTCTCTTAAATGCAAAGAATGTTTCCATGGCCTCTGGATGCAA
ATACACAGAGCTCTGGGGTCAGAGCAAGGGATGGGGAGAGGACCACGAGTGAAAAAGCAGCTACACACATTCAC
CTAATTCCATCTGAGGGCAAGAACAACGTGGCAAGTCTTGGGGTAGCAGCTGTT

13711.1

TCCAGACATGCTCCTGTCTAGCGGGGAGCAGGAACCAGACCTGCTATGGGAAGCAGAAAGAGTTAAGGGAAG
GTTTCCTTTTCATTCCTGTTCTTCTTTTGTCTTTGAACAGTTTTTAAATATACTAATAGCTAAGTCATTTGC
CAGCCAGGTCCCGGTGAACAGTAGAGAACAAGGAGCTTGCTAAGAATTAATTTTGTGTTTTTACCCCATTC
AACAGAGCTGCCCTGTTCCCTGATGGAGTTCATTCCTGCCAGGGCACGGCTGAGTAACACGAAGCCATTCAAG
AAAGGCGGGTGTGAAATCACTGCCACCCCATGGACAGACCCCTCACTCTTCTTCTTAGCCGCAGCGCTACTTA
ATAAATATATTTATACTTTGAAATTATGATAACCGATTTTTCCCATGCGGCATCCTAAGGGCACTTGCCAGCTC
TTATCCGGACAGTCAAGCACTGTTGTTGGACAACAGATAAAGGAAAAGAAAAAGAAAACAACCGCAACTTC
TGT

Fig. 15L

47/101

13711.2

TGAGACGGACCACTGGCCTGGTCCCCCTCATKTGCTGTGCTAGGACCTGACATGAAACGCAGATCTAGTGGCA
GAGAGGAAGATGATGAGGAACCTCTGAGACGTCGGCAGCTTCAAGAAGAGCAATTAATGAAGCTTAACTCAGGC
CTGGGACAGTTGATCTTGAAAGAAGAGATGGAGAAAGAGAGCCGGGAAAGGTCATCTCTGTTAGCCAGTCGCTA
CGATTCTCCCATCAACTCAGCTTCACATATTCATCATCTAAACTGCATCTCTCCCTGGCTATGGAAGAAATG
GGCTTCACCGGCTGTTTCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCAGCGGGGGAGTGCGAGAT
TACCAGACACTTCAGATGGCCACATGCCTGCAATGAGAATGGACCGAGGAGTGCTATGCCAACATGTTGGA
ACCAAAGATATTTCCATATGAAATGCTCATGGTGACCAACAGAGGGCCGAAACCAATCTCAGAGAGGTGGACA
GAA

13713.1&2

TCACTTTATTTTCTTGTATAAAAACCTATGTTGTAGCCACAGCTGGAGCCTGAGTCCGCTGCACGGAGACTC
TGGTGTGGGTCTTGACGAGGTGGTCAGTGAACCTCTGATAGGGAGACTTGGTGAATACAGTCTCCTCCAGAGG
TCGGGGGTGAGGTAGCTGTAGGTCTTAGAAATGGCATCAAAGGTGGCCTTGGCGAAGTTGCCAGGTTGGCAGT
GCAGCCCCGGGTGAGGTGTAGCAGTCATCGATACCAGCCATCATGAG

13715.4

CTGGAATATAGACCCGTGATCGACAAAACCTTTGAACGAGGCTGACTGTGCCACCGTCCCGCCAGCCATTCGCTC
CTACTGATGAGACAAGATGTGGTGATGACAGAATCAGCTTTTGTATTATGTATAATAGCTCATGCATGTGTCC
ATGTCATAACTGTCTTCATACGCTTCTGCACTCTGGGGAAGAAGGAGTACATTGAAGGGAGATTGGCACCTAGT
GGCTGGGAGCTTGCCAGGAACCCAGTGGCCAGGGAGCGTGGCACTTACCTTTGTCCCTTGCTTCATTCTTGTGA
GATGATAAACTGGGCACAGCTCTTAAATAAAATATAAATGAACA

13717.1&2

TGAATGGGGAGGAGCTGACCCAGGAAATGGAGCTTGNGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAG
TGGGCATCTGTGGTGGTGCCTCTTGGGAAGGAGCAGAAGTACACATGCCATGTGGAACATGAGGGGCTGCCTGA
GCCCCCTACCCCTGAGATGGGGCAAGGAGGAGCCTCCTTCATCCACCAAGACTAACACAGTAATCATTGCTGTTT
CGGTTGTCCTTGGAGCTGTGGTCATCCTTGGAGCTGTGATGGCTTTTGTGATGAAGAGGAGGAGAAACACAGGT
GGAAAAGGAGGGGACTATGCTCTGGCTCCAGGCTCCAGAGCTCTGATATGTCTCTCCAGATTGTAAAGTGTG
AAGACAGCTGCCTGGTGTGGACTTGGTGACAGACAATGTCTTCACACATCTCCTGTGACATCCAGAGACCTCAG
TTCTCTTTAGTCAAGTGTCTGATGTTCCCTGTGAGTCTGCGGGCTCAAAGTGAAGAACTGTGGAGCCCAGTCCA
CCCCTGCACACCAGGACCCTATCCCTGCACTGCCCTGTGTTCCCTTCCACAGCCAACCTTGCTGCTCCAGCCAA
ACATTGGTGGACATCTGCAGCCTGTCAGCTCCATGCTACCCTGACCTTCAACTCCTCACTTCCACACTGAGAAT
AATAATTTGAATGTGGGTGGCTGGAGAGATGGCTCAGCGTGACTGCTCTTCAAAGGTCTGAGTTCAAATCC
CAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATCTAATACCCTCTTCTGCAGTGTCTGAAGACASCT
ACAGTGTACTTACATATAATAATAAATAAG

Fig. 15M

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13719.1&2

GGCCGGGCGCGCGCGCCCCGCCACACGCACGCCGGGCGTGCCAGTTTATAAAGGGAGAGAGCAAGCAGCGAGT
CTTGAAGCTCTGTTTGGTGCTTTGGATCCATTTCCATCGGTCCTTACAGCCGCTCGTCAGACTCCAGCAGCCAA
GATGGTGAAGCAGATCGAGAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAACTTGTAGTAG
TTGACTTCTCAGCCACGTGGTGTGGGCCTTGCAAAATGATCAAGCCTTTCTTTCATTCCCTCTCTGAAAAGTAT
TCCAACGTGATATTCTTGAAGTAGATGTGGATGACTGTCAGGATGTTGCTTCAGAGTGTGAAGTCAAATGCAT
GCCAACATTCCAGTTTTTTAAGAAGGGACAAAAGGTGGGTGAATTTTCTGGAGCCAATAAGGAAAAGCTTGAAG
CCACCATTAATGAATTAGTCTAATCATGTTTTCTGAAAATATAACCAGCCATTGGCTATTTAAACTTGTAATT
TTTTTAATTTACAAAAATATAAAATATGAAGACATAAACCCMGTGCCATCTGCGTGACAATAAACATTAATG
CTAACACTT

13721.1

TCACATAAGAAATTTAAGCAAGTTACRCTATCTTAAAAACACAACGAATGCATTTTAATAGAGAAACCTTCC
CTCCCTCCACCTCCCTCCCCACCCTCCTCATGAATTAAGAATCTAAGAGAAGAAGTAACCATAAAACCAAGTT
TTGTGGAATCCATCATCCAGAGTGCTTACATGGTGATTAGGTTAATATTGCCTTCTTACAAAATTTCTATTTTA
AAAAAATTATAACCTTGATTGCTTATTACAAAAAATTCAGTACAAAAGTTCAATATATTGAAAAATGCTTTT
CCCCTCCCTCACAGCACCGTTTTATATATAGCAGAGAATAATGAAGAGATTGCTAGTCTAGATGGGGCAATCTT
CAAATTACACCAAGACGCACAGTGGTTTATTTACCCTCCCCTTCTCATAAG

13721.2

GGAAAGGATTCAAGAATTAGAGGACTTGCTTGCTRRAGAAAAAGACAACCTCTCGTCGCATGCTGACAGACAAAG
AGAGAGAGATGGCGGAAATAAGGGATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAG
TTAGCCCTGGACATGGAAATCAGTGCTTACAGGAACTCTTAGAAGGCGAAGAAGAGAGGTTGAAGCTGTCTCC
AAGCCCTTCTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACCGTACAACCTAGAGGAAAGCGG
AAGAGGGTTGATGTGGAAGAATCAGAGGCGAAGTAGTAGTGTTAGCATCTCTCATTCCGCTCAACCACTGGAA
ATGTTTGCATCGAAGAAATTGATGTTGATGGGAAATTTATCCCGCTTGAAGAACACTTCTGAACAGGATCAACC
AATGGGAAGGCTTGGGAGATGATCAGAAAAATTGGAGACATCAGTCAGTTATAAATATACCTCAA

13723.1

CATGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAACSTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCA
AAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCCAAAGCTGTTTCTTTTGTCTTTAGCGTAAAGCT
CTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGCTCAGTCACTCCGTGGTCTTTTTCTCTTT
CCAGTTCTTCTCTCTCTCTTCAAGTTCTGCCTCAGTGAAAGCTGCAGGTCCCAGTTAAGTGATCAGGTGAGGG
TTCTTTGAACCTGGTTCTATCAGTCGAATTAATCCTTCATGATGG

Fig. 15N

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13723.2

GATGTGTTGGACCTCTGTGTCAAAAAAACCTCACAAAGAAATCCCCTGCTCATTACAGAAGAAGATGCATTTA
AAATATGGGTATTTTTCAACTTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTCAGAAGAGATTGAATAC
CTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAATCAACTT
TGATGACAGTAAAAATGGCCTTTCTGCATGGGAACCTATTGAGCTTATTGGAAATGGACAGTTTAGCAAAGGCA
TGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTAATGAACCTATATTAGATGTGTTAAAGCAGGGT
TACATGATGAAAAAGGGCCACAGACGGAAAAACTGGACTGAAAGATGGTTTGTACTAAAACCCAACATAATTTT
TACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTGGATGAAAATTGCTGTGTAGAAGTCC
TTGCCTGACAAAAGATGGAAAGAAATGCCTTTT

13725.1

GACTGGTTCTTTATTTCAAAAAGACACTTGTCAATATTCAGTRTCAAAACAGTTGCACTATTGATTTCTCTTTT
TCCAATCGGCCCAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGATGTACACCTA
ACAGACCTCTAGAAACCTTACCAGAAAATGGGGACTGGGTAGGGAAGGAACTTAAAGATCAACAACTGCC
AGCCACGGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCAAGCAAAGTTTCAA
AATAATATAAAATTTAAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGATACAAAGCACA
ATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAAGTTTCACATGGCTAA
ATCAGTGGCAAAAACACAGTCTTCTTTCTTTCTTTCTTTCAAGGANGCAGGAAAGCAATTAAGTGGTCACCTTA
ACATAAGGGGGAC

13725.2

TGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGATCCAGGTTCTGCAGCAGCAGGC
AGATGATGCAGAGGAGCGAGCTGAGCGCTCCAGCGAGAAGTTGAGGGAGAAAGCGGGCCCGGAACAGGCTG
AGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTGGACCGTGCTCAGGAGCGCCTG
GCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGAGAGAGGTATGAAGGTTATTGA
AAACCGGGCCTTAAAGATGAAGAAAAGATGGAACCTCAGGAAATCCAACCTCAAAGAAGCTAAGCACATTGCAG
AAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAAGGAGACTTGAACCGCACAGA
AGGAACGAGCTTGAGCTTGGCAAAAGTCCCGTTGCCAGAGATGGGATGAACCAGATTAGACTGATGGACCANA
ACC

13726.1&2

AGGGGCGNGCGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCG
AGAGTGACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTGTCGC
CTGCATTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGTAA
CCCAGAAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGCACCTCGGGCACTC
AAAGAGATTGCGAAATTTGCCATGAAGGAGATGGGAACCTCAGATGTGCGCATTGACACCAGGCTCAACAAAGC
TGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGGTGTGCGGCTGTCCAGAAAACGTAATGAGGAT
GAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGT
CAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAAT

Fig. 150

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13727.1

TCGGGAGCCACACTTGGCCCTCTTCTCTCCAAAGSGCCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCTC
TTGGAGACACAGAGGGTTTACCTTGGATGACCTCTAGAGAAATTGCCAAGAAGCCACCTTCTGGTCCCAAC
CTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGCTGTAGAAGGTCAGTTGGCTCCATTGCCCTGCTTCCAAC
CAATGGGCAGGAGAGAAGGCCTTTATTTCTCGCCACCCATTCTCTGTACCAGCACCTCCGTTTTAGTCAG
TGTTGTCCAGCAACGGTACCGTTTACACAGTCACCTCAGACACACCATTTACCTCCCTTGCCAAGCTGTTAGC
CTTAGAGTGATTGCAGTGAACACTGTTTACACACCGTGAATCCATTCCCATCAGTCCATTCCAGTTGGCACCAG
CCTGAACCATTGGTACCTGGTGTTAACTGGAGTCTGTTACAAGGTGGAGTCGGGGCTTGCTGACTTCTCTT
CATTTGAGGGCAC

13727.2

ACCTAGACAGAAGGTGGGTGAGGGAGGACTGGTAGGAGGCTGAGGCAATTCCTTGGTAGTTTGTCTGAAACCC
TACTGGAGAAGTCAGCATGAGGCACCTACTGAGAGAAGTGCCAGAACTGCTGACTGCATCTGTTAAGAGTTA
ACAGTAAAGAGGTAGAAGTGTGTTCTGAATCAGAGTGAAGCGTCTCAAGGGTCCACAGTGGAGGTCCCTGA
GCTACCTCCCTTCCGTGAGTGGGAAGAGTGAAGCCATGAAGAACTGAGATGAAGCAAGGATGGGGTTCTGGG
CTCCAGGCAAGGGCTGTGCTCTCTGCAGCAGGGAGCCCCACGAGTCAGAAGAAAAGAACTAATCATTTGTTGCA
AGAAACCTTGCCCGGATACTAGCGGAAAAGTGGAGGCGNGGTGGGGGCACAGGAAAGTGGAAGTGATTTGATG
GAGAGCAGAGAAGCCTATGCACAGTGGCGGAGTCCACTGTAAAGTG

13728.1&2

TTCAAGCAATTGTAACAAGTATATGTAGATTAGAGTGAGCAAAATCATATACAATTTTCATTTCCAGTTGCTAT
TTTCCAAATTGTTCTGTAATGTCGTTAAAATTACTTAAAAATTAACAAAGCCAAAAATTATATTTATGACAAGA
AAGCCATCCCTACATTAATCTTACTTTTCCACTACCGGCCCATCTCCTTCCTCTTTTCTAACTATGCCATT
AAAAGTGTCTACTGGGCCGGGCGTGTGGCTCATGCCTGTAATCCAGCATTTTGGGAGGCCAAGGCAGGCGGA
TCATGAGGTCAAGAGATTGAGACCATCCTGGCCAACATGGTGAACCCCGCCTCGACTAAGAATACAAAAATTA
GCTGGGCATGGTGGCGCATGCCTGTAGTCTCAGCTACTCGGGAGGCTGAGGCAGAAGAATCGCTTGAACCCGGG
AGGCAGAGGATGCAGTGAGCCCCGATCGCGCCACTGCACTCTAGCCTGGGCGACAGACTGAGACTCTGCTC

13731.1&2

TGTGCCAGTCTACAGGCCTATCAGCAGCGACTCCTTCAGCAACAGATGGGGTCCCCTGTTTCCAGCCCAACCCCAT
GAGCCCCCAGCAGCATATGCTCCCAAATCAGGCCAGTCCCCACACCTACAAGGCCAGCAGATCCCTAATTCTC
TCTCCAATCAAGTGCCTCTCCCCAGCCTGTCCCTTCTCCACGGCCACAGTCCAGCCCCCCCCACTCCAGTCCT
TCCCCAAGGATGCAGCCTCAGCCTTCTCCACACCAGTTTCCCCACAGACAAGTTCCCCACATCCTGGACTGGT
AGTTGCCCAGGCCAACCCCATGGAACAAGGGCATTGTCAGCC

Fig. 15P

51/101

13734.1&2

TGTA AAAA CTTG TTTT AATTTT GTATA AAAA TAAAGGTGGTCCATGCCACGGGGGCTGTAGGAAATCCAAGCA
GACCAGCTGGGGTGGGGGGATGTAGCCTACCTCGGGGACTGTCTGTCTCAAAACGGGCTGAGAAGGCCCGTC
AGGGGCCCAGGTCCACAGAGAGGCCTGGGATACTCCCCAACCCGAGGGGCAGACTGGGCAGTGGGGAGCCCC
CATCGTGCCCCAGAGGTGGCCACAGGCTGAAGGAGGGGCTGAGGCACCGCAGCCTGCAACCCCCAGGGCTGCA
GTCCACTAACTTTTTACAGAATAAAAGGAACATGGGGATGGGGAAAAAGCACCAGGTGAGGCAGGGCCCGAGG
GCCCCAGATCCCAGGAGGGCCAGGACTCAGGATGCCAGCACCACCCTAGCAGCTCCACAGCTCCTGGCACAGG
AGGCCGCCACGGATTGGCACAGGCCGCTGCTGGCCATCACGCCACATTTGGAGAACTTGTCGCCACAGAGGTCA
GCTCGGAGGAGCTCCTCGTGGGCACACACTGTACGAACACAGATCTCCTTGTTAATGACGTACACACGGCGGAG
GCTGCGGGGACAGGGCACGGGAGGTCTCAGCCCCACTT

13736.2

ATGGCTGCTGGATTTAGGTGGTAATAGGGGCTGTGGGCCATAAATCTGAAGCCTTGAGAACCTTGGGTCTGGAG
AGCCATGAAGAGGGAAGGAAAAGAGGGCAAGTCTGAACCTAACCAATGACCTGATGGATTGCTCGACCAAGAC
ACAGAAGTGAAGTCTGTGTCTGTGCACTTCCACAGACTGGAGTTTTTGGTGCTGAATAGAGCCAGTTGCTAAA
AAATTGGGGGTTTGGTGAAGAAATCTGATTGTTGTGTGATTCAATGTGTGATTTAAAAATAAACAGCAACAA
CAATAAAAACCTGACTGGCTGTTTTTCCCTGTATTCTTTACAACATTTTTTGACCTCTGAAAATTATTAT
ACTTCACCTAAATGGAAGACTGCTGTGTTGTGGAAATTTGTAATTTTTTAATTTATTTTATTCTCTCCTT
TTTATTTTGCTGCAGAATCCGTTGAGAGACTAATAAGGCTTAATATTTAATTGATTTGTTAATATGTATATA
AAT

13744.2-13696.2

GGCATGCGAGCGCACTCGGCGGACGCAAGGGCGGGGAGCACACGGAGCACTGCAGGCGCCGGGTGGGACA
GCGTCTTCGCTGCTGCTGGATAGTCGTGTTTTCGGGGATCGAGGATACTCACCAGAAACCGAAAATGCCGAAAC
CAATCAATGTCCGAGTTACCACCATGGATGCAGAGCTGGAGTTTGCAATCCAGCCAAATACAACCTGGAAAACAG
CTTTTTGATCAGGTGGTAAAGACTATCGGCCTCCGGGAAGTGTGGTACTTTGGCTCCACTATGTGGATAATAA
AGGATTTCTACCTGGCTGAAGCTGGATAAGAAGGTGTCTGCCAGGAGGTGAGGAAGGAGAATCCCTCCAGT
TCAAGTTCGGGGCCAAaGTTCTACCCTGAAGATGTGGCTGAGGAGCTCATCCAGGACATCACCAGAAACTTTT
CTTCCTTCAAGTGAAGGAAGGAATCCTTAGCGATGAGATCTACTGCCCCCTTGARACTGCCGTGCTCTGGGG
TCCTACGCTTGTGCATGCCAAGTTTGGGGACTACCACCAAGAAG

13746.1&2-13720.1&2

GAAGGAGTCGGGATACTCAGCATTGATGCACCCCAATTTCAAAGCGGCATTCTTCGGCAGGTCTCTGGGACAAT
CTCTAGGGTCACTACCTGGAACTCGTTAGGGTACAACCTGAATGCTGAAAGGAAAGAACACCTGCAGAACCGGA
CAGAAATTCACCCCGCGATCAGCTGATTGATCTCGGTGACAGAGTATGGCTAAAGATGACGAGGACGTT
GTCAATTCCTGGGCTTTTGAAGTGAGTCCAGCAGCAGTCTGAGGTATTCGGGCCGTTATGCACCTGGACCA
CCAGCACCAGCTCCCGGGGGGCCAGGTGCCAGCCTTATCTACATTCTCAGGGTCTGATCAAAGTTCAGCTGG
TACACCAGGACCGGTACCGCAGCGTCAGGTTGTCCGCTCGGGCTGGGGGACCGCCGGGACCAGGGAAGCCGCC
GACACGTTGGAGACCTGCGGATGCCACAGCCACAGAGGGGTGGTCCCCACCGCGGCCGCCGGCACCCCGCGC
GGGTTCCGGCTCCAGCAACGGTGGGGCGAGGGCCTCGTTCTTCTTTGTGCCCCATTGCTGCTCCAGAGGACGA
AGCCGCAGGCGGCCACCACGAGCGTCAGGATTAGCACCTTCGGTTTGTAGATGCGGAACCTCATGGTCTCCAGG
GCCGGGAGCGCAGCTACAGCTCGAGCGTCGGCGCCGCCGTAGGAGCCGCGGCTCGGCTTCTGCTCCGTCCTCT
CCATTACGACACACGGGTCCCGGAAAAAGCTCAGCCSCGGTCCCAACCGCACCTAGCTTCGTTACCTGCGCCT
CGCTTG

Fig. 15Q

52/101

14347.1

CAGATTTTATTTGCAGTCGTCAGTGGGGCCGTTTCTTGCTGCTTATTTGTCTGCTAGCCTGCTCTTCCAGCTG
CATGGCCAGGCGCAAGGCCTTGATGACATCTCGAGGGCTGAGAAATGCTTGGCTTGCTGGGCCAGAGCAGATT
CCGCTTTGTTCAAAAGGTCTCCAGGTCATAGTCTGGCTGCTCGGTCATCTCAGAGAGCTCAAGCCAGTCTGGT
CCTTGCTGTATGATCTCCTTGAGCTCTTCCATAGCCTTCTCCTCCAGCTCCCTGATCTGAGTCATGGCTTCGTT
AAAGCTGGACATCTGGGAAGACAGTTCCTCCTCTTCTTGATAAATTGCCTGGAATCAGCGCCCCGTTAGAGC
AGGCTTCCATCTCTTCTGTTTCCATTTGAATCAACTGCTCTCCACTGGGCCCACTGTGGGGGCTCAGCTCCTTG
ACCCTGCTGCATATCTTAAGGGTGTTAAAGGATATTCACAGGAGCTTATGCCTGGT

14347.2

CTCCTCTTGGTACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGA
CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTACAGCAAGGCCACTGGTACAGACAATCT
TTGAAGGTGGAAAAGCAACTTGTTTGCATATGGCCAGACAGGAAGTGGCAAGACACATACTATGGGCGGAGAC
CTCTCTGGGAAAGCCCAGAATGCATCAAAGGGATCTATGCCATGGCCTTCCGGGACGTCTTCTTCTGAAGAAT
CAACCCTGCTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGA
CCTGCTCAACAAGAAGGCCAAGCTTGCGCGTGCTGGAAGACGGCAAGCAACAGGTGCAAGTGGTGGGGGCTTGC
AGGAACATCTGGNTAACTCTGCTTGATGATGGCANTCAAGATGATCGACATGGGCAGCGCCTGCAGA

14348.2&14350.1&2

TCCCGAATTC AAGCGACAAATTGGAWAGTGAAATGGAAGATGCCTATCATGAACATCAGGCAAATCTTTTGCGC
CAAGATCTGATGAGACGACAGGAAGAATTAAGACGCATGGAAGAACTTCACAATCAAGAAATGCAGAAACGTAA
AGAAATGCAATTGAGGCAAGAGGAGGAACGACGTAGAAGAGAGGAAGAGATGATGATTTCGTCAACGTGAGATGG
AAGAACAAATGAGGCGCCAAAGAGAGGAAAGTTACAGCCGAATGGGCTACATGGATCCACGGGAAAGAGACATG
CGAATGGGTGGCGGAGGAGCAATGAACATGGGAGATCCCTATGGTTCAGGAGGCCAGAAATTTCCACCTCTAGG
AGGTGGTGGTGGCATAGGTTATGAAGCTAATCCTGGCGTTCCACCAGCAACCATGAGTGGTTCATGATGGGAA
GTGACATGCGTACTGAGCGCTTTGGGCAGGGAGGTGCGGGGCTGTGGGTGGACAGGGTCTAGAGGAATGGGG
CCTGGAATCCAGCAGGATATGGTAGAGGGAGAGAAGGTACGAAGGC

14349.1&2

TTCGTGAAGACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCCGAGTGACACCATTGAGAATGTCAAGG
CAAAGATCCAAGACAAGGAAGGCATCCCTCCTGACCAGCAKAGGTTGATCTTTGCTGGGAAACAGCTGGAAGAT
GGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGAT
GCAATCTTCGTGAAGACCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCCAGTGACACCATCGAGAATG
TCAAGGCAAAGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTG
GAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTGCGCTTGAGGGG
GGGTGTCTAAGTTTCCCTTTTAAGGTTTCAACAAATTCATTGCACTTTCCTTTCAATAAAGTTGTTGCATTC

Fig. 15R

53/101

14352.1&2

GCGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCGAGAGT
GACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTGTCGCCTGCA
TTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGTAACCCGA
GAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGACCTCGGGCACTCAAAGA
GATTCGGAAATTTGCCATGAAGGAGATGGGAAGTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCT
GGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGAT
TCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTACCCTTTCAAAAATCTACAGACAGTCAATGT
GGATGAGAACTAATCGCTGATCGT

14353.1

AATTCTTTATTTAAATCAACAACTCATCTTCTCAAGCCCCAGACCATGGTAGGCAGCCCTCCCTCTCCATCC
CCTCACCCACCCCTTAGCCACAGTGAAGGGAATGGAAAATGAGAAGCCACGAGGGCCCTGCCAGGGAAGGCT
GCCCCAGATGTGTGGTGAGCACAGTCAGTGCAGCTGTGGCTGGGGCAGCAGCTGCCACAGGCTCCTCCCTATAA
ATTAAGTTCTGCAGCCACAGCTGTGGGAGAAGCATACTTGTAGAAGCAAGGCCAGTCCAGCATCAGAAGGCAG
AGGCAGCATCAGTGACTCCCAGCCATGGAATGAACGGAGGACACAGAGCTCAGAGACAGAACAGGCCAGGGGGA
AGAAGGAGAGACAGAATAGGCCAGGGCATGGCGGTGAGGGA

14353.2

TGATGAATCTGGGTGGGCTGGCAGTAGCCGAGATGATGGGCTCTTCTCTGGGGATCCCAACTGGTTCCTAAG
AAATCCAAGGAGAATCCTCGGAACCTCTCGGATAACCAGTGCAGAGGGCAAGAACGTGATCGGGTTACAGAT
GGGCACCAACCGCGGGGCGTCTCANGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATCCCACC
CCAGGCCTTGCCCTGCCCTCCCACGAATGGTTAATATATATGTAGATATATATTTAGCAGTGACATTCCCAG
AGAGCCCCAGAGCTCTCAAGCTCCTTTCTGTGAGGGTGGGGGTTCAAGCCTGTCTGTACCTCTGAAGTGCC
TGCTGGCATCCTCTCCCCATGCTTACTAATACATTCCCTTCCCATAGCC

17182.1&2

AGCGGAGCTCCCTCCCCTGGTGGCTACAACCCACACACGCCAGGCTCAGGCATCGAGCAGAAGTCCAGCGACTG
GGTAACCACTGACATTCAGGTGAAGGTGCGGGACACCTACCTGGATACACAGGTGGTGGGACAGACAGGTGTCA
TCCGCAGTGTACGGGGGGCATGTGCTCTGTGTACCTGAAGGACAGTGAGAAGGTTGTCAGCATTTCCAGTGAG
CACCTGGAGCCTATCACCCCAACGAACAAGGTGAAAGTGATCCTGGGCGAGGATCGGGAAGCCACGGG
CGTCTACTGAGCATTGATGGTGAGGATGGCATTGTCCGTATGGACCTTGATGAGCAGCTCAAGATCCTCAACC
TCCGCTTCTGGGGAAGCTCCTGGAAGCCTGAAGCAGGCAGGCGCGGTGGACTTCGTGGATGAAGAGTGATCC
TCCTTCTTCCCTGGCCCTTGGCTGTGACACAAGATCCTCCTGCAGGGCTAGGCGGATTGTTCTGGATTTCTT
TTGTTTTCTTTTAGGTTTCCATCTTTTCCCTCCCTGGTGCTCATTGGAATCTGAGTAGAGTCTGGGGGAGGG
TCCCCACCTTCTGTACCTCCTCCACAGCTTGCTTTTGTGTACCGTCTTCAATAAAAAGAAGCTGTTTGG
TCTA

Fig. 15S

54/101

17183.2

GGTTCACAGCACTGCTGCTTGTGTGTTGCCGGCCAGGAATTCAGGCTCACAAAGGCTATCTTAGCAGCTCGTTC
TCCGGTTTTTAGTGCCATGTTTGAACATGAAATGGAGGAGAGCAAAAAGAATCGAGTTGAAATCAATGATGTGG
AGCCTGAAGTTTTTAAGGAAATGATGTGCTTCATTTACACGGGGAAGGCTCCAAACCTCGACAAAATGGCTGAT
GATTTGCTGGCAGCTGCTGACAAGTATGCCCTGGAGCGCTTAAAGGTCATGTGTGAGGATGCCCTCTGCAGTAA
CCTGTCCGTGGAGAACGCTGCAGAAATTCATCCTGGCCGACCTCCACAGTGCAGATCAGTTGAAAACCTCAGG
CAGTGGATTTTCATCAACTATCATGCTTCGGATGTCTTGGAGACCTCTTGGG

17186.1&2

TCGTAGCCATTTTTCTGCTTCTTTGGAGAATGACGCCACACTGACTGCTCATTGTCGTTGGTTCCATGCCAATT
GGTGAAATAGAACCTCATCCGGTAGTGGAGCCGGAGGGACATCTTGTCATCAACGGTGATGGTGCGATTTGGAG
CATACCAGAGCTTGGTGTTCTCGCCATACAGGGCAAAGAGGTTGTGACAAAGAGGAGAGATACGGCATGCCTGT
GCAGCCCTGATGCACAGTTCCTCTGCTGTGTACTCTCCACTGCCCGAGCCGGAGGGGCTCCCTGTCCGACAGATA
GAAGATCACTTCCACCCCTGGCTTG

17187.1&2

TGGCACACTGCTCTTAAGAACTATGAWGATCTGAGATTTTTTTGTGTATGTTTTTGACTCTTTTGAGTGGTAA
TCATATGTGTCTTTATAGATGTACATACCTCCTTGACAAATGGAGGGGAATTCATTTTCATCACTGGGAGTGT
CCTTAGTGTATAAAAAACCATGCTGGTATATGGCTTCAAGTTGTAATAATGAAAGTGACTTTAAAAGAAAATAGG
GGATGGTCCAGGATCTCCACTGATAAGACTGTTTTTAAGTAACTTAAGGACCTTTGGGTCTACAAGTATATGTG
AAAAAATGAGACTTACTGGGTGAGGAAATTCATTGTTTTAAAGATGGTCGTGTGTGTGTGTGTGTGTGTGTG
TTGTGTTGTGTTTTGTTTTTAAGGGAGGGAATTTATTATTTACCGTTGCTTGAAATTACTGKGTAAATATATG
TYTGATAATGATTTGCTYTTTGVMACCTAAAATTAGGVCTGTATAAGTWCTARATGCMTCCTGGGKGTGATY
TTCCMAGATATTGATGATAMCCCTTAAAATTGTAACCYGCCTTTTTCCCTTTGCTYTCMATTAAAGCTATTM
AAAG

17191.1&89.1

GGGGGTAGGCTCTTTATTAGACGGTTATTGCTGTACTACAGGGTCAGAGTGCAGTGTAAAGCAGTGTGAGAGGCC
CGCGTTCAGCCCAAGAATGTGGATTTTCTCTCCCTATTGATCACAGTGGGTGGGTTTCTTCAGAAAAGCCCCAG
AGGCAGGGACCAAGTGAGCTCCAAGGTTAGAAGTGGAACGGGAAGGCTTCAGTCACATGCTGCTTCCACGCTTCC
AGGCTGGGCAGCAAGGAGGAGATGCCCATGACGTGCCAGGTCTCCCATCTGACACCAGTGAAGTCTGGTAGGA
CAGCAGCCGCACGCCTGCCTCTGCCAGGAGGCCAATCATGGTAGGCAGCATTGCAGGGTCAGAGGTCTGAGTCC
GGAATAGGAGCAGGGGCAGGTCCCTGCGGAGAGGCACCTTCTGGCCTGAAGACAGCTCCATTGAGCCCTGCAGT
ACAGGYGTAGTGCTTGGACCAAGCCACAGCCTGGTAAGGGGCGCCTGCCAGGGCCACGGCCAGGAGGCA

Fig. 15T

55/101

17192.1&2

TAATTTCTTAGTCGTTTGAATCCTTAAGCATGCAAAGCTTTGAACAGAAGGGTTCACAAAGGAACCAGGGTT
GTCTTATGGCATCCAGTTAAGCCAGAGCTGGGAATGCCTCTGGGTCTCCACATCAGGAGCAGAAGCACTTGAC
TTGTCGGTCCTGCTGCCACGGTTTGGGCGCCACCACGCCACGTCCACCTCGTCCTCCCTGCCGCCACGTCC
TGGGCGGCCAAGGTCTCCAAAATTGATCTCCAGCTGAGACGTTATATCATTGCTGGCTTCGGAAATGATGGT
CCATAACCGAATCTTCAGCATGAGCCTCTTCACTCTTTGATTATGAAGAACAAATCCCTTCTTCCACTGCCCA
TCAGCACCTTCATTGTTTTGGATATTAAATTCTACTTTTGGCCGGTCTTATTTGAATAGCCTTCCACTC
ATCCAAAGTCATCTCTTTGGACCCTCTCTTTACCTCTTCAACTTCATTCTCCTTATTTTCAGTGTCTGCCA
CTGGATGATGTTCTTCACTTCAGGTGTTTCTCAGTCACATTTGATTGATCCAAGTCAGTTAATTCGTCTTTG
ACAGTTCCCCAGTTGTGAGATCCGCTACCTCCACGTTTGTCTCGTGCTTCAGGCCAGATCTATCACTTCCACT
ATGCCTATCAAATTCACGTTTGGCACGAGAATCAAATCCATCTCCTCGGCCATTCCACGTCCACGGCCCCCTC
GACCTCTTCCAAGACCACCACGACCTCGAATAGGTGCGTCAATAATCGGTCTATCAACTGAAAATTCGCCTCT
TCACCTTTTCTTCAAGTGGCTTTTGAATCTTCGTTACGAGGTGGTGCCTTTCTGGTCTTCTATCAATTAT
TTTCCCTTACCCTGAAGTTGTTGATCAGGTCTTCTTCCAACCTCGTGC

17193

AAGCGGATGGACCTGAGTCAGCCGAATCCTAGCCCCTTCCCTTGGGCCTGCTGTGGTGCTCGACATCAGTGACA
GACGGAAGCAGCAGACCATCAAGGCTACGGGAGGCCCGGGGCGCTTGCGAAGATGAAGTTTGGCTGCCTCTCCT
TCCGGCAGCCTTATGCTGGCTTTGTCTTAAATGGAATCAAGACTGTGGAGACGCGCTGGCGTCTCTGCTGAGC
AGCCAGCGGAACGTACCATCGCCGTCCACATTGCTCACAGGGACTGGGAAGGCGATGCCTGTGGGAGCTGCT
GGTGGAGAGACTCGGGATGACTCCTGCTCAGATTAGGCCTTGCTCAGGAAAGGGGAAAAGTTTGGTCGAGGAG
TGATAGCGGGACTCGTTGACATTGGGGAACTTTGCAATGCCCCGAAGACTTAACTCCCGATGAGGTTGTGGAA
CTAGAAAATCAAGCTGCACTGACCAACCTGAAGCAGAAGTACCTGACTGTGATTTCAAACCCAGGTGGTTACT
GGAGCCCATACCTAGGAAAGGAGGCAAGGATGTATTCCAGGTAGACATCCAGAGCACCTGATCCCTTTGGGGC
ATGAAGTGTGACAAGTGTGGGCTCCTGAAAGGAATGTTCCRGAGAAACCAGCTAAATCATGGCACCTTCAATTT
GCCATCGTGACGCAGACCTGTATAAATTAGGTAAAGATGAATTTCACTGCTTTGGAGAGTCCCACCCACTAA
GCACTGTGCATGTAACAGGTTCTTTGCTCAGATGAAGGAAGTAGGGGTGGGGCTTTCTTGTGTGATGCCT
CCTTAGGCACACAGGCAATGTCTCAAGTACTTTGACCTTAGGGTAGAAGGCAAAGCTGCCAGTAAATGTCTCAG
CATTGCTGCTAATTTTGGTCTGCTAGTTTCTGGATTGTACAAATAAATGTGTTGTAGATGA

Fig. 15U

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16443.1.edit

TCGAGCGGCCCGCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGACCTGGTTCTT
GGTCATCTCCTCCCGGGATGGGGGCAGGGTGACACCTGTGGTCTCGGGGCTGCCCTTTGGCTTTGGAGATGG
TTTTCTCGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTA CTCTTGCCATTCAACCAGTCCTGG
TGCANGACGGTGAGGACGCTNACCACACGGTACGNGCTGGTGTACTGCTCCTCCCGCGGCTTTGTCTTGGCATT
ATGCACCTCCACGCCGTCCACGTACCAATTGAACCTGACCTCAGGGTCTTCGTGGCTCACGTCCACCACCACGC
ATGTAACCTCAAANCTCGGNCGCGANCACGC

16443.2.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTC
CAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC TACAAGACCACGCCTCCCGTGC
TGGACTCCGACACCTGCCGGGCGGCCGCTCGA

16444.2.edit

AGCGTGGTTNCGGCCGAGGTCCCAACCAAGGCTGCANCCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACT
GGTGAGACCTGCGTGTACCCCACTCAGCCCACTGTGGCCAGAAAGTGGTACATCAGCAAGAACCCCAAGGA
CAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACC
CTGCCGATGTGGACCTGCCCGGGCGGNCGCTCGA

16445.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAA
GAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGA
CTGGTGAGACCTGCGTGTACCCCACTCAGCCCACTGTGGCCAGAAAGTGGTACATCAGCAAGAACCCCAAG
GACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGA
CCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

Fig. 15V

57/101

16445.2.edit

TCGAGCGGTCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGNCATGCTCTCGCCGAACCAGACATGCCTCTTGNCCTTGGGGTTCTTGCTGATGTACCAGNTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCANTCTCCATGTTGCANAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGACAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGTTCTTGACCTCGGTCGCGACCACGCT

16446.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCTCTCAGAGCGGTAGCTGTTCTTATTGCCCCGGCAGCCTCCATAGATNAA
GTTATTGCANGAGTTCTCTCCACGTCAAAGTACCAGCGTGGGAAGGATGCACGGCAAGGCCAGTGACTGCGT
TGGCGGTGCAGTATTCTTCATAGTTGAACATATCGCTGGAGTGGACTTCAGAATCCTGCCTTCTGGGAGCACTT
GGGACAGAGGAATCCGCTGCATTCTGCTGGTGGACCTCGGCCGCGACCACGCT

16446.2.edit

AGCGTGGTCGCGGCCGAGGTCCACCAGCAGGAATGCAGCGGATTCTCTGTCCCAAGTGCTCCAGAAGGCAGG
ATTCTGAAGACCACTCCAGCGATATGTTCAACTATGAAGAATACTGCACCGCCAACGCAGTCACTGGGCCTTGC
CGTGCATCCTTCCACGCTGGTACTTTGACGTGGAGAGGAACCTCTGCAATAACTTCATCTATGGAGGCTGCCG
GGGCAATAAGAACAGCTACCGCTCTGAGGAGGACCTGCCCGGGCGGCCGCTCGA

16447.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAATGGCACATCTTGAGGTCACGGCANGT
GCGGGCGGGTTCTTGACCTCGGCCGCGACCACGCT

Fig. 15W

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16447.2.edit

AGCGTGGTTCGCGGCCGAGGTCAAGAAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGGCTGGA
AGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAG
ACTGGTGAGACCTGCCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAACTGGTACATCAGCAAGAACCCCAA
GGACAAGAGGCATGTCTGGCTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCG
ACCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

16449.1.edit

AGCGTGGTTCGCGGCCGAGGTCTGTGAGAGTGGCACTGGTAGAAGNTCCAGGAACCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGNAATGGGGCCCATGANATGGTTGN
CTGAGAGAGAGCTTCTTGTCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGNGG
GCGGTGNGGTCCGCCTAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCANAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGG
AACATCCAAGATCTCTGNTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGCTGTCTTTT
CCTTCCAATCANGGGCTCGCTCTTCTGAATATTCTCAGGGCAATGACATAAATTGTATATTGGTTCCCGGTT
CCAGGCCAG

16450.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCAACTGGTAACCTTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCTGGGTATG
ACACTGGAATGGTATTACGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAN
GAACATGGNTTTAGGCGGACCACACCGGCCACAACGGGCACCCCATAGGCATAGGCCAAGAACATACCCGNC
GAATGTAGGACAAGAAGCTCTNTCTCANACAANCATCTCATGGGCCCATTCANGACACTTCTGAGTACATCA
NTTCATGGCATCCTGGTGGCACTGATAAAACCCCTACAGTTA

16450.2.edit

AGCGTGGTTCGCGGGCGAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGTCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGTGG
GCGGTGTGGTCCGCCTAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGG
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGTCTGTCTTTT
TCCTTCCAATCANGGGCTCGCTCTTCTGATTATTCTCAGGGCAATGACATAAATTGTATATTGGNTCCCGG
TNCAGCCAATAATAAACCTCTGTGACACCANGGCGGGGCCGAAGGANCAT

Fig. 15X

59/101

16451.1.edit

AGCGTGGTCGCGGCCGAGGTCTCACCAGAGGTACCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTGCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGA
CAATGGTGTGAACATAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTC
GA

16451.2.edit

TCGAGCGGCCGCGGCCGAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTCGTTCCCACTCATCTCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGNTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCTCCACTATGATGTTGTAGGTGGTACCTCTGGTGAGGACCTCGGCCGCGACCAG
CT

16452.1.edit

AGCGTGGCGCGGCCGAGGTCCATTGGCTGGAACGGCATCAACTTGAAGCCAGTGATCGTCTCAGCCTTGTT
CTCCAGCTAATGGTGATGGNGGTCTCAGTAGCATCTGTACACGAGCCCTTCTTGGTGGGCTGACATTCTCCAG
AGTGGTGACAACACCTGAGCTGGTCTGCTTGTCAAAGTGCCTTAAGAGCATAGACACTCACTTCATATTTGG
CGNCCACCATAAGTCTGATACAACCACGGAATGACCTGTGAGGAAC

16452.2.edit

TCGAGCGGCCGCGGCCGAGGTCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGACGATGAT
ATGGAGAGCCAGCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCACCTCAGGT
CACACCCACAAGCCTGAGCGCCAGTGGACACCACCAATGTTTCAGCTCACTGGATATCGAGTGCGGGTGACCC
CCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTT
ATGGCGGCCACCAATATGAAGTGAAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT
TGTCACCACTCTGGAGAATGTCAGCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCA
TTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGACCTCGGCCG
CGACCACGCTT

Fig. 15Y

60/101

16453.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCCGAACCTGCCAGTGTACAGGGAAGATGTACATGTTATAGNTCTTCTCGAA
GTCCCGGGCCAGCAGCTCCACGGGGTGGTCTCCTGCCTCCAGGCGCTTCTCATTCTCATGGATCTTCTTCACCC
GCAGCTTCTGCTTCTCAGTCAGAAGGTTGTTGTCTCATCCCTCTCATACAGGGTGACCAGGACGTTCTTGAGC
CAGTCCCGCATGCGCAGGGGGAATTCGGTCAGCTCAGAGTCCAGGCAAGGGGGGATGTATTTGCAAGGCCGAT
GTAGTCCAAGTGGAGCTTGTGGCCCTTCTTGGTGCCCTCCAAGGTGCACTTTGTGGCAAAGAAGTGGCAGGAAG
AGTCGAAGGTCTTGTGTCATTGCTGCACACCTTCTCAAACCTCGCCAATGGGGGCTGGGCAGACCTGCCCGGC
GGCCGCTCGA

16453.2.edit

TCGAGCGGCCCGCCGGGCAGGTCTGCCAGCCCCCATTGGCGAGTTTGAGAAGGNGTGCAGCAATGACAACAAG
ACCTTCGACTCTTCTGCCACTTCTTTGCCACAAAGTGCACCCTGGAGGGCACCAGAAGGGCCACAAGCTCCA
CCTGGACTACATCGGGCCTTGCAAATACATCCCCCTTGCTGGACTCTGAGCTGACCGAATTCCTTCTGCGCA
TGCGGGACTGGCTCAAGAACGTCTGGTCACCCTGTATGAGAGGGATGAGGACAACAACCTTCTGACTGAGAAG
CANAAGCTGCGGGTGAAGANATCCATGAGAATGANAAGCGCCTGNAGGCANGAGACCCCGTGGAGCTGCT
GGCCCGGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTCGGCCAGACCTCGGCCG
CGACCACGCT

16454.1.edit

AGCGTGGNTGCGGACGACGCCACAAAGCCATTGTATGTAGTTTTANTTCAGCTGCAAANAATACCNCCAGCAT
CCACCTTACTAACCAGCATATGCAGACA

16454.2.edit

TCGAGCGGTGCGCCGGGCAGGTCTGGGCGGATAGCACCAGGCATATTTTGAATGGATGAGGTCTGGCACCTG
AGCAGCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGGTTCTGAGTCT
GTGGGATAGCTGCCATGAAGNAACCTGAAGGAGGCGCTGGCTGGTANGGGTTGATTACAGGGCTGGGAACAGCT
CGTACACTTGCCATTCTCTGCATATACTGGNTAGTGAGGCGAGCCTGGCGCTCTTCTTTCGCTGAGCTAAAGC
TACATACAATGGCTTTGNGGACCTCGGCCGCGACCACGCTT

Fig. 15Z

61/101

16455.1.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGACACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGC
CTCTGCTGGTCTTTCAAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCA
CGCT

16455.2.edit

AGCGTGGTTTGC GGCCGAGGTCTCACCANAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGC
AGAGGCATAAGGTTCCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGAT
GACTCGTGCTTTGACCCCTACACAGNTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGG
CTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTGAGATGTGATTCATCTANATGGTGTCATG
ACAATGGTGNGAACTACAAGATTGGAGAGAAGTGGNACCGTCAGGGGANAAAAATGGACCTGCCCGGGCGGCNCG
CTCGA

16456.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCTTNCTGCTCANGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGG
CTATGCCCTGNATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATC

16456.2.edit

TCGAGCGGCCGCCGGGCAGGTCCAATTGAAACAACAGTTCTGAGACCGTTCTTCACCACTGATTAAGAGTG
GGGNGCGGGTATTAGGGATAATATTCATTTAGCCTTCTGAGCTTTCTGGGCAGACTTGGTGACCTTGCCAGCT
CCAGCAGCCTTCTGGTCCACTGCTTTGATGACACCCACCGCAACTGTCTGTCTCATATCACGAACAGCAAAGCG
ACCCAAAGGTGGATAGTCTGAGAAGCTCTCAACACACATGGGCTTGCCAGGAACCATATCAACAATGGGCAGCA
TCACCAGACTTCAAGAATTTAAGGGCCATCTTCAGCTTTTTACCAGAACGGCGATCAATCTTTTCCTTCAGCT
CAGCAAACCTGCATGCAATGTGAGCCG

Fig. 15AA

62/101

16459.1.edit

TCGAGCGGCCGCCGGGCAGGTCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCT
GGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTTGNTAC
TGACCCAGGGCTGACCACCAGCCTCTCAGGAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACA
CAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACTCAGNNGGGTTTGAT
GTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTGAACACCCATGGGANGNCATGC
CTGATCTGGACTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAACAGGCTGNTTGCTGANAAAGCAAGTGA
CCAAGGANGAAATTTCANGGGTGAAANGGACTGCTCCCGCTCCTGAATTCAGTCTACTCAACCTGANGNTGCA
GACTGGTCTTGAAGNGNACANGGGCCCTCTGGGCCTATTTAAGCANTTCGGTCGCGAACACGNT

16459.2.edit

AGCGTGNGTCGCGGCCGAGGTGCTGAATAGGCACAGAGGGCACCTGTACACCTTCAGACCAGTCTGCAACCTCA
GGCTGAGTAGCAGTGAACCTCAGGAGCGGGAGCAGTCCATTACCCTGAAATTCCTCCTTGGNCACTGCCTTCTC
AGCAGCAGCCTGCTCTTCTTTTCAATCTCTTCAGGATCTCTGTAGAAGTACAGATCAGGCATGACCTCCCATG
GGTGTTCACGGGAAATGGTGCCACGCATGCGCAGAATTCCTCGAGCCAGCATCCACCACATCAAACCCACTGAG
TGAGCTCCCTTGTTGTTGCATGGGATGGGCAATGTCCACATAGCGCAGAGGAGAATCTGTGTTACACAGCGCAA
TGGTAGGTAGGTTAACATAAGATGCCCTCCGCGAGAAGCTGGTGGTCAGCCCTGGGGTCAAGTAACCACAAGAAG
CCGTGGCTCCCGGAAGGCTGCCTGGATCTGGTTAGTGAAGNTCCAGGAGTGAAGCGGCCAACAATTGGAGTGG
CTTCAGTGGCAAGCAGCAAACTTCAGCACAAGCCCTCTGGACCTGCCCCGGCGCCGCTCGA

16460.1.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTTCTCCCTGACGGNCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCNTCCCCGAACCTTATGC
CTCTGCTGGGCTTTCAGNGCCTCCACTATGATGNTGTAGGGGGGCACCTCTGGNGANGACCTCGGCCGCGACCA
CGCT

16460.2.edit

AGCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGCTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGGTCAATTCAGATGTGATTCATCTAGATGGTGCCATG
ACAATGGNGNGAACTACAAGATTGGAGAGAAGTGGNACCGNCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCT
CGA

Fig. 15BB

63/101

16461.1.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGNTGCA
ACCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAGTGGCACATCTTGAGGTACGGCAGGTGC
GGNCGGGGNTTTTGCGGCTGCCCTCTGGNCTTCGGNTGTNCTCNATCTGCTGGCTCA

16461.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTCGCGGTGCGACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGG
ACCTCCTGGCCCCCTGGTCCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGG
CTCAGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC
ACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGCAGNCGCAAGAACCCCGCCGCAC
CTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGCTGCAA
CCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGG
CCAAAAGAAGTGGTACATCAGCAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCGGCGAGAACATGACCGAT
GGATTCCAGTTCGAGTATGGCGGGCAGGGCTCCGACCCTGCCGATGGGGACCTTGCCCGGAACACGCT

16463.1.edit

AGCGTGGNNGCGGCCGAGGTATAAATATCCAGNCCATATCCTCCCTCCACACGCTGANAGATGAAGCTGTNCAA
AGATCTCAGGGTGGANAAAACCAT

16463.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTTCAGACTTGGACTGTGTCACTGCCAGGCTTCAGGGCTCCAACCTTGC
AGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACACCATGGTT
TTATCCACCCTGAGATCTTTGAACAATTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATATTTCTAC
CTCGGCCGCGACCACGCT

Fig. 15CC

64/101

16464.1.edit

CGAGCGGGCGACCGGGCAGGTNCAGACTCCAATCCANANAACCATCAAGCCAGATGTCAGAAGCTACACCATCA
CAGGTTTACAACCAGGCACTGACTACAAGANCTACCTGCACACCTTGAATGACAATGCTCGGAGCTCCCTGTG
GTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCT
GGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGTACATCATCNAGTATGANAAGCCTGGGCCTCCTCCAG
AGAAGNGGTCCCTCGGCCCGCCCTGNTGTCCANAGGNTACTATTACTGNGCCNGCAACCGGCAACCGATATC
NATTTTGNCATTGGCCTTCAACAATAATTA

16464.2.edit

AGCGTGGTTCGCGGCCGANGTCCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCCTGAACTGTAAGGGTTC
TTCATCAGNGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTG
TCTGAGAGAGAGCTTCTTGNCCTGTCTTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCA
ATGACATAAATTGTATATTGGGTCCCGGNTCCAGGCCAGTAATAGTANCCTCTGTGACACCAGGGCGGNGCCG
AGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTAACCGGTAATCCTGGCACGTGGCG
GCTGCCATGATACCAGCAAGGAATTGGGTGTGGTGGCCAGGAAACGCAGGTTGGATGGNGCATCAATGGCAGT
GGAGGCCGTCGATGACCACAGGGGGAGCTCCGACATTGTCATTCAAGGTG

16465.1.edit

AGCGTGGNCGCGGCCGAGGTGCAGCGCGGGCTGTGCCACCTTCTGCTCTCTGCCCAACGATAAGGAGGGTNCCT
GCCCCAGGAGAACATTAACNTCCCCAGCTCGGCCTCTGCCGG

16465.2.edit

TCGAGCGGCCGCCCGGGCAGGTTTTTTTTGCTGAAAGTGGNTACTTTATTGGNTGGGAAAGGGAGAAGCTGTGG
TCAGCCCAAGAGGGAATACAGAGNCCGAAAAAGGGGAGGGCAGGTGGGCTGGAACCAGACGCAGGGCCAGGCA
GAACTTTCTCTCTCACTGCTCAGCCTGGTGGTGGCTGGAGCTCANAAATTGGGAGTGACACAGGACACCTTC
CCACAGCCATTGCGGCGGCATTTTCATCTGGCCAGGACACTGGCTGTCCACCTGGCACTGGTCCCGACAGAAGCC
CGAGCTGGGGAAGTTAATGTTACCTGGGGGCAGGAACCTCCTTATCATTGNGCAGAGAGCAGAAGGTGGCA
CAGCCCGCTGCACCTCGGCCGCGACCACT

16466.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCATAAGTCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGAT
TTCTTTCATTGGTCCGGNCTTCTCCTTGGGGGNCACCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGCG
TCCACTGGGCGCTCAGGCT

16467.2.edit

TCGAGCGGTTCCGCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGA
TTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGCGGTCCCTCGGCCCGCCCTGGT
GTCACAGAGGCTACTATTACTGGCCTGGAACCGGAACCGAATATACAATTTATGTCATTGNCCTGAAGAATAA
TCANNAANAGCGANCCCTGATTGGAAGGA

Fig. 15DD

66/101

06_16471.edit

AGCGTGGTCGCGGCCGAGGTCTGCTGCTTCAGCGAAGGGTTTCTGGCATAACCAATGATAAGGCTGCCAAAGAC
TGTTCCAATACCAGCACCAGAACCAGCCACTCCTACTGTTGCAGCACCTGCACCAATAAATTTGGCAGCAGTAT
CAATGTCTCTGCTGATTGCACTGGTCTGAAACTCCCTTTGGATTAGCTGAGACACACCATTCTGGGCCCTGATT
TTCCTAAGATAGAACTCCAACCTTTGCCCTCTAGCACATAGCCATCTGCTCGGTCACTGTCCCGGCTTGA
AGCGATGCACGCAAGAAGCTTGCCCTGCTGGAAGTCTCTCCAGGAGACTGCTGATTTTGGCATTCTTTTCC
TTTCATCATATTTCTTCTGAATTTTTTTAGATCGTTTTTTGTTTAAATCTCTTCTTCTCAGGAGTCAGCTTG
GCCCCCGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGG
AATTTCTCCTGGGGCTCAGAGTGGTGTACTCGTAAACAAGGATCATCGATGGTGNCTACAATGCATCTAATAA
CGAGCTGGGTGCGACCCAAAGAACCTGGNGAANAATGGATCGNCTCATCGACAGGACACCGTACCCGACAGGG
GNACGANTCCCACTATGCGCTTGCCCTGGGCGCAANAAAGGAAAAGTGGCGGGCGGCCNTCGAAAGCCCAA
TTNTGGAAAAATCCATCACACTGGGNGGCCNGTCGAGCATGCATNTANAGGGGCCCATTCCCCCTNANN

07_16472.edit

TCGAGCGGCCCGCCGGGCAGGTCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAG
ACTGGTGAGACCTGCGTGTAACCCACTCAGCCAGTGTGGCCAGAAGAACTGGTACATCAGCAAGAACCCCAA
GGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCG
ACCTTGCCGATGTGGACCTCGGCCGCGACACGCT

08_16472.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCTGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCGAACCAGACATGCCTCTTGCTCTGGGGTTCTTGCTGATGTACCAGTCTTCTGGGCCACA
CTGGGCTGAGTGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGTTGGGGACCTGCCCGGGCGGCCGCTCGA

09_16473.edit

TCGAGCGGCCCGCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCCTTCACACCCCAA
TCTTCATGGACCAGAGATCTTGATGTTCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCTGGGTATG
ACACTGGAATGGTATTAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAG
GAACATGGNTTTAGGCGGACCACACCGCCCAACGGCCACCCCATAGGCATAGGCCAAGACCATACCCGCC
GAATGTAGGACAAGAAGCTNTNTNTCANACACCATNTNATGGGCCCCATTCCAGGACACTTCTGAGTACATCAT
TTATGNCATCTGTGGCACTTGATGAAAACCTTACAGTTCAGGGTTCTGGAATTTTACCAGGCCTNTTACAGG
ACTNGGCCGGACNCCTTAAGCCNATTNACCCCTGGGGCGTTCTANGGTCCCACTCGNNCACTGGNGAAAAATGGC
TACTGTN

Fig. 15FF

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11_16474.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC
GAGGTTGTGGTGTCTGNGAACTCCNAGGACANGAGGGCTAAATTCCATGAAGTTTGTGGATGGCCTGATGATC
CACAATCGGAGACCCTGTTAACTACTACCGTCTNACCNCCTGCTGTNCNCCCCNTTCTGCTNAANACATNGG
GNTNNTNCTTGNCNTCCTTGGGTNGAANATNNAATNGCCTNCCNTTNTANCNCTACTNGNTCCANANTTGG
CCTTTAAANAATCCNCCTTGCTTNNNCACTGTTCANNTNTTTNNTCGTAAACCTATNANTTNNATTANATNN
TNNNNNNCTACCCCCCTCNTATTNANCCNATANGCTNNNAANTCCTTNANNCTCCCNCCNNTNCNCTCNT
ACTNANTNCTTCTNCCCATTACNAGCTCTTTCTTTAANATAATGNNGCCNNGCTCTNCATNTCTACNATNT
GNNNAATNCCCCNCCCCNANCGNNTTTTGACCTNNNAACCTCCTTTCTCTTCCCTNCNNAATNTNCNNAN
TTCNCNTTCCNNTTTTCGGNTNNTCCCATNCTTCCANNCTTCANTCTANCNCNCTNCAACTTATTTTCT
NTCATCCCTTNTTCTTTACANNCCCCTNNTCTACTCNCNNTTNCATTANATTTGAACTNCCACNNTANTT
NCCTCNCCTACNNTTTTATTTTNCGNTCNCCTACNTAATANTTTAATNANTTNTCN

12_16474.edit

TCGAGCGGCCGCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGACTGGCTGGGGCATGGCAGGCG
GCTCTGGCTTCCACCCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC
ACGTGGTCAGGCAGGGGCTTCTTAGGGCAATCTTACCAGTTGGGTCCCAGGGCAGCATGATCTTCACCTTGAT
GCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAAGCAGTGTCAACGTAGTAAGTTAACAGGGTCTCCGCT
GTGGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCCTCGGAGTTTCCAGACACCACAACCT
CGCAGCCTTTGGCCCCACTCTCCATGATGAACCGCAGCACACCATAGCAGGCCCTCCGCACAAGCAAGCCCTCC
TAAGAATTTGTAACGCANANACTCTGCTGGCAATGGCACACAAACCTCTAGTGGACCTCGGNCGCGACCACGC

13_16475.edit

TCGAGCGGCCGCCCGGGCAGGTCTGGTCCAGGATAGCCTGCGAGTCCTCCTACTGCTACTCCAGACTTGACATC
ATATGAATCATACTGGGAGAATAGTTCTGAGGACCAGTAGGGCATGATTCACAGATTCCAGGGGGGCCAGGAG
AACCAGGGGACCCTGGTTGTCTGGAATACCAGGGTCACCATTTCTCCAGGAATACCAGGAGGGCCTGGATCT
CCCTTGGGGCCTTGAGGTCTTGACCATTAGGAGGGCGAGTAGGAGCAGTTGGAGGCTGTGGGCAAACTGCACA
ACATTCTCCAAATGGAATTTCTGGGTTGGGGCAGTCTAATCTTGATCCGTCACATATTATGTCATCGCAGAGA
ACGGATCCTGAGTCACAGACACATATTTGGCATGGTTCTGGCTTCCAGACATCTCTATCCGNCATAGGACTGAC
CAAGATGGGAACATCCTCCTTCAACAAGCTTNTGTTGTGCCAAAAATAATAGTGGGATGAAGCAGACCGAGAA
GTANCCAGCTCCCTTTTTGCACAAAGCNTCATCATGTCTAAATATCAGACATGAGACTTCTTTGGGCAAAAAA
GGAGAAAAAGAAAAAGCAGTTCAAAGTANCCNCCATCAAGTTGGTTCTTGCCNTTCAGCACCCGGGCCCGT
TATAAACACCTNNGGCCGACCCCCCTT

Fig. 15GG

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14_16475.edit

AGCGTGGTCGCGGCCGAGGTGTTTTATGACGGGCCCGGTGCTGAAGGGCAGGGAACAACCTTGATGGTGCTACTT
TGAAGTGCCTTTCTTTCTCCTTTTGCACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTTGTGCA
AAAGGGGAGCTGGCTACTTCTCGCTCTGCTTCATCCCACTATTATTTTGGCACAAACAGGAAGCTGTTGAAGGAG
GATGTTCCCATCTTGGTCAGTCCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTGTCTGT
GACTCAGGATCCGTTCTCTGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCCAACCCAGAAATTC
ATTTGGAGAAATGTTGTGCAGTTTGGCCACAGCCTCCAAGTCTCTACTCGCCCTCCTAATGGTCAAGGACCTC
AAGGCCCCAAGGGAGATCCAGGCCCTCCTGGTATTCTGGGAGAAATGGTGACCTGGTATTCCAGGACAACCA
GGGTCCCCTGGTTCTCTGGCCCCCTGGAATCNGGNGAATCATGCCCTACTGGTCTCAAACCTATTCTCCCAN
ATGATTCATATGATGTCAAGTCTGGGATAGCNAGTANGGANGGACTCGCAGGCTATTCTGGACCANACCTGCC
GGGGGGCGTTTCAAAGCCGAATCTGCANANNTNCNTTCACTGGCGGCCGTGAGCTGCTTTAAAAGGGCCA
TTCNCCTTTAGNGNGGGGANTACAATTACTNGGCGGCGTTTTANANCGCGNGNCTGGGAAAT

15_16476.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGGTTGGGGTCAATCCAGTACTCTCCTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGTGC
GGGCGGGTCTTGGCGGTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCTCAGGCTCTTGAGGGTGGTG
TCCACCTCGAGGTACGGTCACGAACCACATTGGCATCATCAGCCCGGTAGTAGCGGCCACCATCGTGAGCCTT
CTCTTGANGTGGCTGGGGCAGGAAGTGAAGTCAAACAGCGCTGGGAGGACCAGGGGGACCAANAGGTCCAGG
AAGGGCCCGGGGGGACCAACAGGACCAGCATCACCAGTGCGACCCGCGAGAACCTGCCCGGCCGNCCTCG
AA

16_16476.edit

TCGAGCGNCGCCCGGGCAGGTCTCGCGGTGCGACTGGTGATGCTGGTCTGTGGTCCCCCGGCCCTCCTGG
ACCTCCTGGTCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCTGCCCCAGCCACCTCAAGAGAAGC
CTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCTGTGACCGTGACCTCGAGGTGGACACC
ACCTCAAGAGCCTGAGCCAGCAGATCGAGAATCCTGGAGCCCAGAGGGCAGCCGAAGAACCCCGCCGCAC
CTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCA
ACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTC
GCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCTGGCGAGAGCATGACCGA
TGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCACCTGCGGATGTGGACCTCCGGCCGCGACCACCTT

Fig. 15HH

69/101

17_16477.edit

TNGAGCGGCCGCCGGGAGGNTGNNACGCTGGTCCTGCTGGTCCTCCTGGCAAGGCTGGTGAAGATGGTCAC
CCTGGAAAACCCGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCCTGGTGGTTTCCCTGGAACCTCC
TGGACTTCCTGGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCCGGTGCTCCTG
GTGTGAAGGGTGAACCTGGTGCCCTGGTGAAAATGGAACCTCAGGTCAAACAGGAGCCCGTGGGCTTCCTGGT
GAGAGAGGACCGTGTGGTGCCCTGGCCCANACCTCGGCCGCGACCACGCTAAGCCGAATTTCCAGCACACT
GGNGGCCGTTACTANTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGNGTGA
AATTGTTATCCGCTCACAATTTACACANCATACGAAGCCGGAAAGCATAAAGTGTAAGCCTTGGGGTGCTAA
TGAGTGAGCTAACTCNCATTAAATTGCGTTGCGCTCACTGCCGCTTTTCCANNNGGAAACCNNTGGCNTNGCC
NGCTTGCTTAANTGAAATCCGCCNACCCCGGGGAAAGNCGGTTTGCNGTATTGGGGCNCCTTTTCCCTTTTC
CTCGGNTTACTTGANTTANTGGGCTTTGGNCGNTTCGGGTTGNGGCGANCNGGTTCAACNTCACNCCAAAGGNG
GNAANACGGTTTTCCANAATCCGGGGGNTANCCCAANGNAAAACATNNGNCNAANGGGCT

18_16477.edit

AGCGTGGTTNGCGGCCGAGGTCTGGGCCAGGGGCACCAACACGTCCTCTCTCACCAGGAAGCCACGGGCTCCT
GTTTGACCTGGAGTTCCATTTTACCAGGGGCACAGGTTCAACCTTACACCAGGAGCACCAGGGCTGTCCTT
CAATCCATNCAGACATTGTGNCCCTAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCCAGGGAAACCACCGA
GCACCTGTGGTCCAACAACCTCTCTCACCAGGTCGTCCGGGTTTTCCAGGGTGACCATCTTACCAGCCTT
GCCAGGAGGACCAGCAGGACCAGCGTTACCAACCTGCCCGGGCGGCCGCTCGA

21_16479.edit

TCGAGCGGCCGCCGGGAGGTCCATTTTCTCCCTGACGGTCCCACCTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCAGCA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCAG
CT

22_16479.edit

AGCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTCGGGAAGAGGTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAAGATGTGATTATCTAGATGGTGCCATG
ACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCCGGCCGC
TCGA

Fig. 15II

70/101

24_16480.edit

TCGAGCGNNCGCCCGGGCAGGTCCAGTAGTGCTTCGGGACTGGGTTACCCCCAGGTCTGCGGCAGTTGTCAC
AGGCCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGCCACTGTTCT
CCTACGTGGTATGTCTTCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCCTTTTCCGTT
CCCAAGACATGTGCAGCTCATTTGGCTGGCTCTATAGTTTGGGGAAAGTTTGTGAAACTGTGCCACTGACCTT
TACTTCCTCCTTCTCTACTGGAGCTTTCGTACCTTCCACTTCTGCTGTTGGTAAAATGGTGGATCTTCTATCAA
TTTCATTGACAGTACCCACTTCTCCCAAACATCCAGGGAAATAGTGATTCAGAGCGATTAGGAGAACCAAATT
ATGGGGCAGAAATAAGGGGCTTTTCCACAGGTTTCTTTGGAGGAAGATTTCACTGGTGACTTTAAAGAATA
CTCAACAGTGTCTTCATCCCCATAGCAAAAGAAGAAACNGTAAATGATGGAANGCTTCTGGAGATGCCNNCATT
TAAGGGACNCCCAGAACTTCACCATCTACAGGACCTACTTCAGTTTACANNAAGNCACATANTCTGACTCANAA
AGGACCCAAGTAGCNCCATGGNCAGCACTTTCAGCCTTCCCTGGGGAAAANNTTACNTTCTTAAANCCTNNG
CCNNGACCCCTTAAGNCCAAATTNTGGAAAANTTCCNTNCNNCTGGGGGGCNGTTCNACATGCNTTTNAAGGG
CCCAATTNCCCNCT

25_16481.edit

TCGAGCGGCCCGCCCGGGCAGGTGTGCGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTGCTGGGATAGAAGCCTTTGACCAGGCAGGTCAAGGCTGACCTGGTTCTT
GGTCATCTCCTCCCGGGATGGGGGCAGGGTGACACCTGTGGTTCTCGGGGCTGCCCTTTGGCTTTGGAGATGG
TTTTCTCGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTACTCCTTGCCATTGAGCCAGTCCTGG
TGCAGGACGGTGAGGACGCTGACCACACGGTACGTGCTGTTGTACTGCTCCTCCCGGGCTTTGTCTTGGCATT
ATGCACCTCCACGCCGTCCACGTACAGTTGAACCTTGACCTCAGGGTCTTCGTGGCTCACGTCCACCACCACGC
ATGTAACCTCAGACCTCGGCCGCGACCACGCT

26_16481.edit

AGCGTGGTTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTC
CAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAAGCCCCGAGAACCACAGGTG
TACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTA
TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGC
TGGACTCCGACACCTGCCCGGGCGGCCGCTCGA

27_16482.edit

TCGAGCGGCCCGCCCGGGCAGGTTGAATGGCTCCTCGCTGACCACCCGGTGTGGTGGTGGGTACAGAGCTCCG
ATGGGTGAAACCATTGACATAGAGACTGTCCCTGTCCAGGGTGTAGGGGCCAGCTCAGTGATGCCGTGGGTCA
GCTGGCTCAGCTTCCAGTACAGCCGCTCTCTGTCCAGTCCAGGGCTTTTGGGGTCAAGGACGATGGGTGCAGACA
GCATCCACTCTGGTGGCTGCCCCATCCTTCTCAGGCCTGAGCAAGGTGAGTCTGCAACCAGAGTACAGAGAGCT
GACACTGGTGTCTTGAACAAGGGCATAAGCAGACCCTGAAGGACACCTCGGCCGCGACCACGCT

Fig. 15JJ

71/101

28_16482.edit

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTCTGCTCTG
TACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCAC
CCATCGTCCTGACCCCAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACG
GCATCACTGAGCTGGGCCCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCT
GTACCCACCACCAGCACCGGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

29_16483.edit

AGCGTGGTCGCGGCCGAGGTCTGTCTCAGAGTGGCACTGGTAGAAGTTCAGGAACCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGCTTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGTGG
GCGGTGTGGTCCGCCTAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGTCTTTTGAAGTGTGGAAGG
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGAAGCTCGTCTGTCTTTT
TCCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACATAAATTGTATATTGCGTCCCGGTT
CCAGGCCAGTAATAGTAGCTCTGTGACACCAGGGCGGGCCGAGGGACCTTCTNTTGAAGAGACCAGCTTC
TCATACTTGATGATGAGNCCGGTAATCCTGGCACGTGGNGGTTGCATGATNCCACCAAGGAAATNGGNGGGGGN
GGACCTGCCCGGGCGGCCGTTCNAAAGCCCAATTCACACACTTGGNGGCCGTACTATGGATCCCACTCNGTCCA
ACTTGGNGGAATATGGCATAACTTTT

31_16484.edit

TCGAGCGGCCGCGGCCGAGGTCTTGACCTTTTCAGCAAGTGGGAAGGTGTAATCCGTCTCCACAGACAAGGC
CAGGACTCGTTTGATCCCGTTGATGATAGAATGGGGTACTGATGCAACAGTTGGGTAGCCAATCTGCAGACAGA
CACTGGCAACATTGCGGACACCCTCCAGGAAGCGAGAATGCAGAGTTTCTCTGTGATATCAAGCACTTCAGGG
TTGTAGATGCTGCCATTGTGCAACACCTGCTGGATGACGACCCAAAGGAGAAGGGGGAGATGTTGAGCATGTT
CAGCAGCGTGGCTTCGCTGGCTCCCACTTTGTCTCCAGTCTTGATCAGACCTCGGCCGCGACCACGCT

37_16487.edit

AGCGTGGTCGCGGCCGAGGTCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA
GTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCTCTTCCCCCGCATCCCCCTTCAAACCTGCCCGGGCGGCCGCTCG

Fig. 15KK

72/101

38_16487.edit

CGAGCGGCCGCCCGGGCAGGTTTGAAGGGGGATGCGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTCA
GGTGCTGGGCACGGTGGGCATGTGTGAGTTTTGTACAAGATTTGGGCTCAACTCTCTTGCTCCACCTTGGTGTT
GCTGGGCTTGTGATCTACGTTGCAGGTGTAGGCTGGGTGCCGAAGTTGCTGGAGGGCACGGTCACCAAGCTGC
TGAGGGAGTAGAGTCCTGAGGACTGTAGGACAGACCTCGGCCGCGACCAAGCT

39_16488.edit

NGGNNGGTCCGGNCNGNCAGGACCACTCNTCTTCGAAATA

41_16489.edit

AGCGTGGTCGCGGCCGAGGTCCTCACTTGCTCCTGCAAAGCACCGATAGCTGCGCTCTGGAAGCGCAGATCTG
TTTTAAAGTCCTGAGCAATTTCTCGCACCAGACGCTGGAAGGGAAGTTTGCGAATCAGAAGTTCAGTGGACTTC
TGATAACGTCTAATTTACGGAGCGCCACAGTACCAGGACCTGCCCGGGCGGCCGCTCGA

42_16489.edit

TCGAGCGGCCGCCCGGGCAGGTCCTGGTACTGNGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAAC
TTCTGATTCGAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCTGCGCTTC
CAGAGCGCAGCTATCGGTGCTTTCAGGAGGCAAGTGAGGACCTCGGCCGCGACCAAGCT

45_16491.edit

TCGAGCGGCCGCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGGTTCTTGACCTCGGCCGCGACCAAGCT

Fig. 15LL

73/101

46_16491.edit

GTGGGNTTGAACCCNTTTNANCTCCGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGA
ATTCGGCTTAGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCGCACCTGCCGTGACCTCAAGATGTGCCACTC
TGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCA
ACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAAGTGTGGCCAGAAGAACTGGTACATCAGCAAG
AACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCA
GGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

47_16492.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCGCAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCCAGGACAACAGCATTAG
TGTCAAGTGGCTGCCTTCAAGTTCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGAC
CAACAAAACTAAAAGTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCACAGTGGAGTAT
GTGGTTAAGTGTCTATGCTCAGAATCCAAGCGGAGAGAAGTCAGCCTCTGGTTCAGACTGNAAGTAACCAACAT
TGATCGCCTAAAGGACTGGCATTCACTGATGNGGATGCCGATTCCATCAAATTGNTTGGGAAAACCCACAGGG
GCAAGTTTNCANGTCNAGGNGGACCTACTCGAGCCCTGAGGATGGAATCCTTGACTNTTCTTNNCCTGATGGG
GAAAAAAACCTTNAAACTTGAAGGACCTGCCCGGGCGCCGTNCAAAACCCAATTCCACCCCTTGGGGGCG
TTCTATGGGNCCCACTCGGACCAAACTTGGGGTAAN

48_16492.edit

TCGAGCGGCCGCCCCGGGCAGGTCTTGAGCTCTGCAGTGTCTTCTTACCATCAGGTGCAGGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCTGTGGGCTTTCCCAAGCAATT
TTGATGGAATCGGCATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTTGTGGTCTGGTCCATTTTTGGGAGTGGTG
GTTACTCTGTAACAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGCTCTGAACATCGGT
CACTTGCATCTGGGATGGTTTGTCAATTTCTGTTCCGTAATTAATGGAAATTGGCTTGCTGCTTGCAGGGGCTTG
TCTCCAGGGCAGTGACAGCATACACAGTGATGGTATAATCAACTCCAGGTTTAAGCCGCTGATGGTAGCTGAA
ACTTTGCTCCAGGCACAAGTGAACCTCTGACAGGGCTATTTCTTCTGTTCTCCGTAAGTGATCCTGTAATATC
TCACTGGGACAGCAGGANGCATTCCAAAACCTCGGGCGNGACCCCTAAGCCGAATTNTGCAATATNCATCACA
CTGGCGGGGCTCGANCATTCAATAAAAGGCCAATCNCCCCATAGGGAGTNTANTACAATTNG

Fig. 15MM

74/101

49_16493.edit

TCGAGCGGCCGCCCGGGCAGGTCACCTTTTGGTTTTTGGTCATGTTCCGGTTGGTCAAAGATAAAACTAAGTTTG
AGAGATGAATGCAAAGGAAAAAATATTTTCAAAGTCCATGTGAAATTGTCTCCCATTTTTTTGGCTTTTGAG
GGGGTTCAGTTTGGGTTGCTTGTCTGTTTCCGGGTTGGGGGAAAGTTGGTTGGGTGGGAGGGAGCCAGGTTGG
GATGGAGGGAGTTTACAGGAAGCAGACAGGGCCAACGTCG

55_16496.edit

AGCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTCCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGA
CAATGGTGTGAACCTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTC
GA

56_16496.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCAG
CT

59_16498.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCATAAGTCCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGAT
TTCTTTTCATTGGTCCGGTCTTCTCCTTGGGGGTCACCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGTG
TCCACTGGGCGCTCAGGCTTGTGGGTGTGACCTGAGTGAACCTCAGGTCAGTTGGTGCAGGAATAGTGGTTACT
GCAGTCTGAACCAGAGGCTGACTCTCTCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGG
CTGCAAGCCTTCAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTTGTGGTCTGGTCCATTTT
TGGGAGTGGTGGTACTCTGTAACCAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGTCC
TGAACATCGGTCACTTGATCTGGGATGGTTTGNCAATTTCTGTTCCGTAATTAATGGAAATTGGCTTGCTGCT
TGCGGGGCTGTCTCCACGGCCAGTGACAGCATACACAGNGATGGNATNATCAACTCCAAGTTTAAGGCCCTGAT
GGTAACTTTAACTTGCTCCAGCCAGNGAAGCTTCCGGACAGGGTATTTCTTCTGGTTTTCCGAAAGNGANCCT
GGAATNNTCTCCTTGGANCAGAAGGANCNTCCAAAACCTGGGCCGGAACCCCTT

Fig. 15NN

75/101

60_16473.edit

AGCGTGGTCGCGGCCGAGGTCTGTGTCAGAGTGGCACTGGTAGAAGTTCCAGGAACCTGAACTGTAAGGGTTCT
TCATCAGTGCCAAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGTCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTGTGG
GCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGG
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGTCTGTCTTTT
TCCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACATAAATTGTATATTCGGTTCCTGGT
TCCAGGCCAGTAATAGTAGCCTCTTGTGACACCAGGCGGGGCCANGGACCACTTCTCTGGGANGAGACCCAGC
TTCTCATACTTGATGATGTAACCCGGTAATCCTGCACGTGGCGGCTGNCATGATACCANCAAGGAATTGGGTGN
GGNGGACCTGCCCGGCGGCCCTCNA

60_16498.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTTCAGGACAACAGCATTAG
TGTCAGTGGCTGCCTTCAAGTTCCTGTTACTGGTTACAGAGTAACCACCACTCCAAAAATGGACCAGGAC
CAACAAAACTAAAAGTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGACAGCCACAGTGGAGTAT
GTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCACTATTCC
TGCACCAACTGACCTGAAGTTCACTCAGGTACACCCACAAGCCTGAGCCGCCAGTGGACACCACCCAATGTTT
ACTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCCATGAAAGAAATCAACCTTGCTCCT
GACAGCTCATCCNGGGGTGTATCAGGACTTATGGGGGACTGCCCCGGCNGGCCGNTCGAAANCGAATTNTGAAA
TTTCTTCNCACTGGGNGGCCGNTTCGAGCTTNTTNTANANGGCCCAATTCNCCTNTAGNGGGTCGTN

61_16499.edit

AGCGTGGTCGCGGCCGAGGTCTNAGGA

62_16483.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCAACTGGTAACCTTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAAGACCCCTTCGTACCCACCTGGGTATG
ACACTGGAATGGTATTAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAG
GAACATGGTTTAGGCGGACCACACCGCCACAACGGGCACCCCAATAAGGNATAGGCCAAGACCATACCCCGC
CGAATGTAGGACAAGAAGCTCTNTCTCAACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCA
TTTCATGTCATCCTGGTGGGCACCTGATGAANAACCTTACAGTTCAGGGTTCCTGGAACCTTACCAGNGCCA
CTTCTGACAGGANCTTGGGCGNGACCACCT

Fig. 1500

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63_16500.edit

AGCGTGGTCGCGGCCGAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCATTG
TCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAA
GCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCAGGAGT
CATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCCTC
TGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTGCCCCGGCGGCCCGCT
CGA

64_16493.edit

AGCGTGGTCGCGGCCGAGGTGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAA
CTCCCTCCATCCCAACCTGGCTCCCTCCCAACCACTTTCCCCCAACCCGAAACAGACAAGCAACCCA
AACTGAACCCCTCAAAGCCAAAAAATGGGAGACAATTTACATGGACTTTGGAAAATATTTTTTCTTTG
CATTATCTCTCAAACCTAGTTTTATCTTTGACCAACCGAACATGACCAAAACCAAAAGTGACCTGCCGGG
CGGCCGCTCGA

64_16500.edit

TCGAGCGGCCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAG
CAGAGGCATAAGGTTGCGGAAGAGGTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGA
TGACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAG
GCTTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTCATCTAGATGGTGCCAT
GACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTCGGCCGCGACCACG
CT

Fig. 15PP

77/101

16501.edit

TCGAGCGGCCCGCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACACTGAACTTCACCATCAACAACC
TGCGGTATGAGGAGAACATGCAGCACCCCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTTCAGGGCCTG
CTCAGGTCCTGTTCAGAGCACCAGTGTGGCCCTCTGTAATCTGGCTGCAGACTGACTTTGCTCAGACCTGA
GAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCTTGATCCCACTGGTNCCTGGACTGGACA
NANAGCGGCTATACTTGGGAGCTGANCCNAACCTTTGGCGGNGACNCCNCTT

16501.2.edit

GAGGACTGGCTCAGCTCCCAGTATAGCCGCTCTCTGTCCAGTCCAGGACCAGTGGGATCAAGGCGGAGGGTGCA
GATGGCGTCCACTCCAGTGGCTGCCCCATGTTTCTCAAGTCTGAGCAAAGNCAGTCTGCAGCCAGAGTACAGAG
GGCCAACACTGGTGCTCTTGAACAGGGACCTGAGCAGGCCCTGAAGGACCCTCTCCGTGGTGTGAACTTCCTG
GAGCCAGGGTGCTGCATGTTCTCTCATACCGCAGGTTGTTGATGGTGAAGTTCAGTGTGAATGGCTCCTCGCT
GACCACCC

16502.1.edit

AGCGTGGTCGCGGCCGAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTA
CCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTC
ACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCA
GAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCAATC
TTCATGGACCANANANCTTGGATNGTCCTTTCACNGGTTNAAAAAACCTTTTCGCCCCCCCACCTTGGGGATT
AACCTTGGGAAANGGGGATTTNACCNCTTC

16502.2.edit

TCGAGCGGCCCGCCGGGCAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCCTGAACTGTAAGGGTT
CTTCATCAGTGCCAACAGGATGACATGAAATGATGTAATCAGAAAGTGTCTGGAATGGGGCCCATGAGATGGTT
GTCTGAGAGAGAGCTTCTTGTCCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGT
GGGCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCAGAAG
TGCCAGGAAGCTGAATACCATTTCCAGTGTATACCCAGGNGGGTGACCAAAGGGGGTCNNTTNGACCTGGNG
AAAGGAACCATCCAAAANCTCTGNCCCATG

Fig. 15QQ

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16503.1.edit

AGCGTGGNCGCGGCCGAGGTCTGAGGATGTAACTCTTCCAGGGGAAGGCTGAAGTGTGACCATGGTGCTAC
TGGGTCCTTCTGAGTCAGATATGTGACTGATGNGAACTGAAGTAGGTACTGTAGATGGTGAAGTCTGGGTGTCC
CTAAATGCTGCATCTCCAGAGCCTTCCATCATTACCGTTTCTTCTTTTGCTATGGGATGAGACACTGTTGAGTA
TTCTCTAAAGTCACCACTGAAATCTTCTCCAAAGGAAAACCTGTGGAAAAGCCCCCTATTTCTGCCCCATAAT
TTGGTTCTCCTAATCNCCTGAAATCACTATTTCCCTGGAANGTTTGGGAAAAANNGGGCNACCTGNCANTGGA
AANTGGATANAAAGATCCCACCATTTTACCCAACNAGCAGAAAGTGGGAANGGTACCGAAAAGCTCCAAGTAAN
AAAAAGGAGGGAAGTAAAGGTCAAGTGGGCACCAGTTTCAAACAAAACCTTCCCCAACTATANAACCCA

16503.2.edit

AAGCGGCCGCCCCGGGCAGGNNCAGNAGTGCCTTCGGGACTGGGNTCACCCCCAGGTCTGCGGCAGTTGTCACAG
CGCCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGCCACTGTTCTCC
TACGTGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCTCCTTTTCCGTTCC
CAAGACATGTGCAGCTCATTTGGCTGGCTCTATAGTTTGGGGAAAGTTGTGAAACTGTGCCACTGACCTTTA
CTTCCTCCTTCTCTACTGGAGCTTTCGGTACCTTCCACTTCTGCTGNTGGNAAAAAGGGNGGAACNTCTTATCA
ATTTCAATTGGACAGTANCCCNCTTTCTNCCCCAAACATNCAAGGGGAAAATATTGATTNCNAGAGCGGATTAAGG
ACAACCCNAATTATGGGGGCCAGAAATAAAGGGGGCTTTTCCACAGGTNTTTTCCT

16504.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGCAGGCTATTGTAAGTGTCTGAGCACATATGAGATAACCTGGGCCAAGC
TATGATGTTGATACGTTAGGTGTATTAATGCACTTTTGACTGCCATCTCAGTGGATGACAGCCTTCTCACTG
ACAGCAGAGATCTTCTCACTGTGCCAGTGGGCAGGAGAAAGAGCATGCTGCGACTGGACCTCGGCCGCGACCA
CGCT

16504.2.edit

AGCGTGGTTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCACTGGCACAGTGAGGAAGATCTCTG
CTGTCACTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAGTGCATTTAATACACCTAACGTATCGAACAT
CATAGCTTGGCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCGGGCGGCCG
TCGA

Fig. 15RR

79/101

16505.1.edit

CGAGCGGCCGCCCGGGCAGGTCCAGACTCCAATCCAGAGAACCACCAAGCCAGATGTCAGAAGCTACACCATCA
CAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCTGTG
GTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCT
GGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCA
GAGAAGTGGTCCCTCGGCCCGCCCTGGTGNACAGAAGCTACTATTACTGGCCTGGAACCGGGAACCGAATAT
ACAATTTATGTCATTGCCCTGAAGAATAATCANAAGAGCGAGCCCCTGATTGGAAGG

16505.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGCTGTCTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAA
TGACATAAATTGTATATTCGTTCCCGGTTCCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGGCCGA
GGGACCATTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTANCCGTAATCCTGGCACCGTGGCG
GCTGCCATGATACCAGCAAGGAATTGGGTGTGGTGGCCAAGAAACGCAGGTTGGATGGTGCATCAATGGCAGTG
GAGGCGTCGATNACCACAGGGGAGCTCCGANCAATTGTCATTCAAGGTGGACAGGTAGAATCTTGTAAATCAGGTG
CCTGGTTTGTAACCTG

16506.1.edit

TCGAGCGGCCGCCCGGGCAGGTTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCA
GATCGAGAACATCCGGAGCCAGAGGGCAGCCGCAAGAACCCGCGCACCTGCCGTGACCTCAAGATGTGCC
ACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTC
TGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCCAAGAAGTGGTACATCAG
CAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCGGCGAAAGCATGACCGATGGATTCCAGTTCGAGTATGGCG
GCCAGGGCTCCGACCCTGCCGATGTGGACCTCGGCCGCGACCACGCTAAGCCCGAATTCAGCACACTGGCGGC
CGTTACTAGTGGGATCCGAGCTTCGGTACCAAGCTTGGCGTAATCATGGGNCATAGCTGTTTCTGNGTGAAAA
TGGTATTCCGCTTCACAATTTCCAC

16506.2.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTTCTTGCTGATGTACCAAGTCTTCTGGGCCACA
CTGGGCTGAGTGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGTTGCA
GCCTTGGTTGGGTCAATCCAGTACTCTCAGTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGTGC
GGGCGGGTTCTTGGGCTGCCCTCTGGGCTCCGATGTTCTCGATCTGCTGGCTCAAGCTCTTGAAGGGTGGT
GTCCACCTCGAGGTACGGTCACGAAACCTGCCCGGGCGGCCGCTCGA

Fig. 15SS

80/101

16507.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAA
GAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGA
CTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAGAAGAACTGGTACATCAGCAAGAACCCCAAG
GACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGA
CCCTGCCGATGTGGACCTGCCCGNGCCGNGCCGCTCGAAAAGCCNAATTTCCAGNCACACTTGGCCGGCCGTT
ACTACTG

16507.2.edit

TCGAGCGGCCGCGCCGGGCAGGTCCACATCGGCAGGGTTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGTTCTTGACCTCGGCCGCGACCACGCT

16508.1.edit

CGAGCGGCCGCGCCGGGCAGGTCCCCCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTT

16508.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGCATTCTTCGACTTCTCTCCAGCCGAGCTTCCCAGAACATCACATATCAC
TGCAAAAATAGCATTGCATACATGGATCAGGCCAGTGGAAATGTAAAGAAGGCCCTGAAGCTGATGGGGTCAAA
TGAAGGTGAATTCAAGGCTGAAGGAAATAGCAAATTCACCTACACAGTTCTGGAGGATGGTTGCACGAAACACA
CTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAACACGCAAGGCTGTGAGACTACCTATTGTAGATATTGCA
CCCTATGACATTGGTGGTCTGATCAAGAATTTGGTGTGGACGTTGGCCCTGTTTGCTTTTATAAACCAAACCT
CTATCTGAAATCCCAACAAAAAAATTTAACTCCATATGTGNTCCTCTTGTTCTAATCTTGGCAACCAGTGCAA
GTGACCGACAAAATTCAGTTATTTATTTCCAAAATGTTTGGAAACAGTATAATTTGACAAAGAAAAAAGGATA
CTTCTCTTTTTTTGGCTGGTCCACCAAATACAATTCAAAAGGCTTTTTGGTTTTATTTTTTANCCAATTCAA
TTTCAAATGTCTCAATGGNGCTTATAATAAAATAAACTTTACCCTTNTTTTNTGAT

Fig. 15TT

81/101

16509.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTT CAGGACAACAGCATTAG
TGTC AAGTGGCTGCCTTCAAGTTCCTTGTACTGGTTACAGAAAGTAACCACCACTCCCAAAAATGGACCAGGA
CCAACAAAACTAAAACTGCAGGTCCAGATCAAACAGAAAATGGACTATTGAAGGCTTGAGCCACAGTGGAA
GTATGTGGNTAGGNGTCTATGCTCAGAATCCCAAGCCGGAGAAAGTCAGCCTTCTGGTTTAGACTGCAGTAACC
AACATTGATCGCCCTAAAGGACTGGNCATTCACTTGGATGGTGGATGTCCAATTC

16509.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTTGAGCTCTGCAGNGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAAACTTGCCCCGTGGGCTTTCCCAAGCAATT
TTGATGGAATCGACATCCACATCAGNGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGTCTGNCCCATTTTTGGGAAGTGG
GGGTTACTCTGTAACCAAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGTCTGAACATC
GGTCACTTGATCTGGGGATGGTTTTGACAATTTCTGGTTCGGCAAATTAATGGAAATTGGCTTGCTGCTGGC
GGGCTGNCTCCACGGGCCAGTGACAGCATAC

16510.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCTTGAGCTCTGCAGTGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAAACTTGCCCCGTGGGCTTTCCCAAGCAATT
TTGATGGAATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGNCTGNCCATTTTTGGGGAAGGG
GTGGTTACTCTTGTAACCAAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGGTGGCCTGAACATC
GGTCACTTGATCTGGGATGGTTTGGTCAATTTCTGTTTGGTAATTAATGGGAAATTGGCTTACTGGCTTGCGG
GGGCTGTCTCCACGGNCAGTGACAAGCATACAGGNGATGGGTATAATCAACTCCAGGTTTAAGGCCNCTGAT
GGTA

16510.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGTAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTT CAGGACAACAGCATTAG
TGTC AAGTGGCTGCCTTCAAGTTCCTTGTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGGACCAGGA
CCAACAAAACTAAAACTGCANGGTCCAGATCAAACAGAAAATGACTATTGAAGGCTTGAGCCACAGTGGAG
TATGTGGGTTAGTGTCTATGCTCAGAATNCCAAGCCGGAGAGATCAGCCTCTGGTTCAGACT

Fig. 15UU

82/101

16511.1.edit

TCGAGCGGCCGCCGGGCAGGTCAGCGCTCTCAGGACGTCAACCACCATGGCCTGGGCTCTGCTCCTCCTCACCC
TCCTCACTCAGGGCACAGGGTCCTGGGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCCTGGA
CAGTCAGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGCTTATGAATTTGTCTCCTGGTACCAACA
ACACCCAGGCAAGGCCCCCAAACCTCATGATTTCTGAGGTCACTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCT
CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCANGCTGAGGATGANGCTGATTATTAC
TGGAAGCTCATATGCAGGCAACAACAATTGGGTGTTGGCGGAAGGGACCAAGCTGACCGTNTAAGGTCAAGC
CCAAGGCTTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAAGAAGCTTCAAGCCAACAANGNCACACT
GGGTGTGTCTCATAAGTGGACTTTCTACCC

16511.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTAGCTTCTGTGGGACTTCCACTGCTCAGGCGTCAGGCTCAGGTAGCTGCTG
GCCGCGTACTTGTGTTGCTTTGNTTGGAGGGTGTGGTGGTCTCCACTCCCGCCTTGACGGGGCTGCTATCTGC
CTTCCAGGCCACTGTACGGCTCCCGGGTAGAAGTCACTTATGAGACACACCAGTGTGGCCTTGTTGGCTTGAA
GCTCCTCAGAGGAGGGTGGGAACAGAGTGACCGAGGGGGCAGCCTTGGGCTGACCTAGGACGGTCAGCTTGGTC
CCTCCGCCGAACACCCAATTGTTGTTGCCTGCATATGAGCTGCAGTAATAATCAGCCTCATCTCAGCCTGGAG
CCCAGAGACNGTCAAGGGAGGCCGTGTTTGCCAAGACTTGGAAGCCAGANAAGCGATCAGGGACCCCTGAGGG
CCGCTTTACNGACCTCAAAAAATCATGAATTTGGGGGGCCTTTGCCTGGGNGTTGGTTGGTNACCAGNAAAAACA
AAATTTCATAAAGCACCAACGTCACTGCTGGTTTCCAGTGCANGAANATGGTGAAGTGAANTGTCC

16512.1.edit

AGCGTGGTCGCGGCCGAGGTCCAGCATCAGGAGCCCCGCCTTGCCGGCTCTGGTCATCGCCTTTCTTTTGTGG
CCTGAAACGATGTCATCAATTGCGAGTAGCAGAAGTCCGCTCTCCACTGCTGTCTTATAAGTCTGCAGCTTCAC
AGCCAATGGCTCCCATATGCCAGTTCCTTCATGTCCACCAAAGTACCCGTCTCACCATTTACACCCAGGTCT
CACAGTTCCTGGGTGTGCTTGGCCGAAGGGAGGTAAGTANACGGATGGTGCTGGTCCCACAGTTCGGATC
AGGGTACGAGGAATGACCTCTAGGGCCTGGGCNACAAGCCCTGTATGGACCTGCCCGGGCGGGCCCGCTCGA

16512.2.edit

TCGAGCGGCCGCCGGGCAGGTCCATACAGGGCTGTTGCCAGGCCCTAGAGGNCATTCTTGTACCCTGATCC
AGAAGTGTGGGACCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAAGTGTGAGACC
TGGGGTGTAATGGNGAGACGGGTACTTTGGTGGACATGAAGGAAGTGGGCATATGGGAGCCATTGGCTGNGAA
GCTGCANACTTATAAGACAGCAGTGGAGACGGCAGTTCGCTACTGCGAATTGATGACATCGTTTCAGGCCACA
AAAAGAAAGCGATGACCANAGCCGGCAAGGCGGGGCTTCCTGATGCTGGACCTCGGCCGCCGACCACGCTT

Fig. 15VV

83/101

16514.1.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC
GAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATGGCCTGATGATCCA
CAGCGGAGACCCTGTAACTACTACGTTGACACTGCTGTGCGCCACGTGTTGCTCANACAGGGTGTGCTGGGCA
TCAAGGTGAAGATCATGCTGCCCTGGGACCCANCTGGCAAAAATGGCCCTTAAAAACCCCTTGCCNTGACCACG
TGAACCATTTGTGNGAACCCCAAGATGAANATACTTGCCACCAACCCCCATTC

16514.2.edit

TCGAGCGGCCCGCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGCAGGCG
GCTCTGGCTTCCACCCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC
ACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCCAGGGCAGCATGATCTTCACCTTGAT
GCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAGCAGTGTCAACGTAGTAGTTAACAGGGTCTCCGCTGT
GGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCTCGGAGTTTCCCAAAACACCACAACCTC
GCCAGCCTTTGGGCCCCACTTCTTCATGAATGAAACCGCAGCACACCATTANCAAGGCCCTTCCGCACAGGNAA
GCCCTTCCTAAGGAGTTTTGTAAACGCAAAAACTCTTGCTGGGGCAAATGGGCACACAGACCTNTANTNGGA
CCTTGGNCCGCGAACCACCGCTT

16515.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCCCTCCTGGCAAGGCTGGTGAAGATGGTCACCCTGGAAAACCCGGACGAC
CTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAACCTCTGGACTTCTGGCTTCAAA
GGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCGGTGCTCCTGGTGTGAAGGGTGAACCTGG
NGCCCCTGGTGAAAATGGAACCTCAGGTCAAACAGGAGCCCGNGGGCTTCTGGNGAGAGAGGACGTGTTGGTG
CCCCTGGCCANACCTGCCCGGGCGCCGCTCNAAAAGCCGAAATCCAGNACACTGGCGGCCGNTACTANTGGA
ATCCGAACCTTCGGTACCAAAGCTTGCCGTAATCATGGCCATAGCTTGTTCCCTGGGGNGGAAATTGGTATTCC
GCTNCCAATTCCACACAACATACCGAACCCGAAAGCATTAAAGTGAAAAGCCCTGGGGGGGCTAAATGANG
TGAGCNTAACTCNCATTTAATTGGCGTTGCGCTTCACTGCCCCGCTTTTCCAGTCCGGGNA

16515.2.edit

TCGAGCGGCCCGCCGGGCAGGTCTGGGCCAGGGGCACCAACACGTCTCTCTCACCAGGAAGCCCACGGGCTCC
TGTTTGACCTGGAGTTCATTTTACCAGGGGCACCAGTTTACCCTTCACACCAGGAGCACCGGGCTGTCCCT
TCAATCCATCCAGACCATTTGTGNCCCCAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCCAGGGAACACGA
GCACCCTGTGGTCCAACAACCTCTCTCTCACCAGGTGCTCCGGGTTTTCCAGGGTGACCATCTTCACCAGCCTT
GCCAGGAGGGCCAGACCTCGGCCGCGACCAGCT

Fig. 15WW

84/101

16516.1.edit

ANCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGNCACCTACAACATCATAGTGGAGGCACTGAAAGACCANCA
GAGGCATAAGGTTTCGGGAAGAGG

16516.2.edit

TCGAGCGGCCGCGGCCGAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGTCCACGGTAACAACCTCTTCCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCNGNCCNGAACAAC
GCTTAAGCCCGNATTCTGCAGAATAATCCCATCACACTTGGCGGCCGCTTCGANCATGCATCNTAAAAGGGGCC
CCAATTTCCCCCTTATAAGNGAANCCGTATTTNCCAATTTCACTGGNCCCGCCGNTTTTACAAACGNCGGTGAA
CTGGGGAAAAACCTGGCGGTTACCCAACCTTAATCGCCNTTGGCAGCACAAATCCCCCTTTTCGNCCANCNTG
GGCGTAAATAACCGAAAA

16517.1.edit

ANCGNGGTGCGGCGCGANGTNTTTTTCTTNTTTTTT

16518.1.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGGGNGGTGAGCGTCCTCACCGTCCTGCACCAGAATTGGTTGAATGGCAAGGAGTACAAGNGCAAGGTTTC
CAACAAAGCCNTCCAGCCCCNTCGAAAAAACCATTTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
ACACCCTGCCCCCATCCCGGGAGGAAAAAGANCAANAACCNGGTTGAGCCTTAACCTTGCTTGGTCNAANGCTTTT
TATCCAACGNACTTCCCCNTGGAANTGGGAAAAACCAATGGGCCAANCCGAAAAACAATTACAANAACCCC

16518.2.edit

TCGAGCGGCCGCGGCCGAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTCAGGCTGACCTGGTTCTT
GGTCATCTCTCCCGGATGGGGCAGGTTGAACACCTGGGGTCTCGGGCTTGCCCTTTGGTTTTGAANATG
GTTTTCTCGATGGGGGCTGGAAGGGCTTTGTTGNAACCTTGCACTTGACTCCTTGCCATTACCCAGNCCTGG
NGCAGGACGGNGAGGACNCTNACCACACGGAACCGGGCTGGTGGACTGCTCC

Fig. 15XX

85/101

16519.1.edit

AGCGTGGTCGCGGACGANGTCCTGTCAGAGTGGNACTGGTAGAAGTTCCANGAACCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGNGNCCTGGAATGGGGCCCATGANATGGTTGC
C

16519.2.edit

TCGAGCGGCCGCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCAACTGGTAACCCCTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTCGGCACCCCCCTGGGTATG
AACCTGGGAAAANGGNANTTAANCTTCTCTGGCA

16520.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCGCAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTGAGGACAACAGCATTAG
TGTCAGTGGCTGCCTTCAAGGTNCCCTGGTACTGGGTACAGANTAACCACCACTCCCAAAAATGGACCAGGA
ACCACAAAACCTTAACTGCAGGGTCCAGATCAAACAGAAATGACTATTGAANGCTTGAGCCACAGTGGGA
GTATGNGGGTAGTGNCATGCTTCAGAATCCAAGCGGAAAAANGTCAAGCCTTNTGGGTCAA

16520.2.edit

TCGAGCGGCCGCGGGCAGGTCTTGCACTCTGCAGTGTCTTCTTACCATCAGGTGCAGGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTACCCCTGTACCTGGAACTTGCCCTGTGGGCTTCCCAAGCAATT
TTGATGGAATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGNCTGAAC
CAGAGGCTGACTCTCTCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAANCCTT
CAATAANNCATTTCTGTTTGATCTGGACC

16521.2.edit

TCGAGCGGCCGCGGGCAGGTCTGGTGGGGTCTGGCACACGCACATGGGGGNGTTGNTCTNATCCAGCTGCC
CAGCCCCATTGGCGAGTTTGAGAAGGTGTGCAGCAATGACAACANACCTTCGACTCTTCTGCCACTTCTTT
GCCACAAAGTGACCCCTGGAGGGCACCAAGAAGGGCCACAAGCTCCACCTGGACTACATCGGGCTTGCAAATA
CATCCCCCTTGCTGGACTCTGAGCTGACCGAATTCCCCCTTGCGCATGCGGGACTGGCTCAAGAACCGTCTT
GGCACCTTGTATGANAGGGATGAAGACACNACCC

Fig. 15YY

86/101

16522.1.edit

AGCGTGGTCGCGGCCGAGGTCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA
GTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCCTCTTCCCCCGCATCCCCCTTCCAAACCTGCCGGGCGGCCGCTCGAAAGCCGAATTCCAGCACACT
GGCGGCCGGTACTAGTGGANCCNAACCTTGGNANCCAACCTGGNGGAANTAATGGGCATAANCTGTTTCTGGGGG
GAAATTGGTATCCNGTTTACAATCCCNCACAACATACGAGCCGGAAGCATAAAAGNGTAAAAGCCTGGGGGNG
GCCTANTGAAGTGAAGCTAACTCACATTAATTNGCGTTGCCGCTCACTGGCCCGCTTTTCAGC

16522.2.edit

TCGAGCGGCCGCGCGGCCGAGGTTTGAAGGGGGATGCGGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTC
AGGTGCTGGGCACGGTGGGCATGTGTGAGTTTTGTACAAAGATTTGGGCTCAACTCTCTTGTCCACCTTGGTGT
TGCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGNGCCGAAGTTGCTGGAGGGCACGGTACCACGCTG
CTGAGGGAGTAGAGTCTGAGGACTGTANGACAGACCTCGGCCGNGACCACGCTAAGCCGAATTCTGCAGATAT
CCATCACACTGGCGGCCGCTCCGAGCATGCATTTTAGAGG

16523.1.edit

AGCGTGGNCGCGGACGANGACAACAACCCC

16523.2.edit

TCGAGCGGCCGCGCGGCCGAGNCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTTGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGNACCAGTTCCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGT
GCGGGCGGGTTCTTGACCT

16524.1.edit

AGCGTGGTCGCGGCCGAGGTCCAGCCTGGAGATAANGGTGAAGGTGGTGCCCCGGACTTCCAGGTATAGCTGG
ACCTCGTGGTAGCCCTGGTGAGAGAGGTGAAACTGGCCCTCCAGGACCTGCTGGTTTCCCTGGTGCTCCTGGAC
AGAATGGTGAACCTGGNGGTAAAGGAGAAAGAGGGGCTCCGGNTGANAAAGGTGAAGGAGGCCCTCCTGNATTG
GCAGGGGCCCCANGACTTAGAGGTGGAGCTGGCCCCCTGGCCCCGAAGGAGGAAAGGTGCTGCTGGTCTCTC
TGGGCCACCTGG

Fig. 15ZZ

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16524.2.edit

TCGAGCGGCCGCCGGGCAGGTCTGGGCCAGGAGGACCAATAGGACCAGTAGGACCCCTTGGGCCATCTTTCCC
TGGGACACCATCAGCACCTGGACCGCCTGGTTACCCCTTGTCACCCTTTGGACCAGGACTTCCAAGACCTCCTC
TTTCTCCAGGCATTCTTGCAGACCAGGAGTACCANCAGCACCAGGTGGCCCAGGAGGACCAGCAGCACCCCTT
CCTCCTTCGGGACCAGGGGGACCAGCTCCACCTCTAAGTCCTGGGGCCCTGCCAATCCAGGAGGGCCTCCTTC
ACCTTTCTACCCGGAGCCCCTCTTTCT

16526.1.edit

TCGAGCGGCCGCCGGGCAGGTCCACCGGGATATTCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAA
GGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTTTACCTGGACAGAGTGAGGAGCCTGGAGACCGACAACC
GGAGGCTGGAGAGCAAAATCCGGGAGCACTTGGAGAAGAAGGGACCCAGGTCAGAGACTGGAGCCATTACTTC
AAGATCATCGAGGACCTGAGGGCTCANATCTTCGCAAATACTGCNGACAATGCCCG

16526.2.edit

ATGCGNGGTGCGGCCGANGACCANCTCTGGCTCATACTTGACTCTAAAGNCNTCACCAGNANTTACGGNCATT
GCCAATCTGCAGAACGATGCGGGCATTGTCCGCANTATTTGCGAAGATCTGAGCCCTCAGGNCCTCGATGATCT
TGAAGTAANGGCTCCAGTCTCTGACCTGGGGTCCCTTCTTCTCCAAGTGCTCCCGGATTTTGCTCTCCAGCCTC
CGGTTCTCGGTCTCCAAGNCTTCTCACTCTGTCCAGGAAAAGAGGCCAGGCGGNCGATCAGGGCTTTTGCATGG
ACT

16527.1.edit

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Fig. 15AAA

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Fig. 15BBB

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Fig. 15CCC

90/101

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Fig. 15DDD

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Fig. 15EEE

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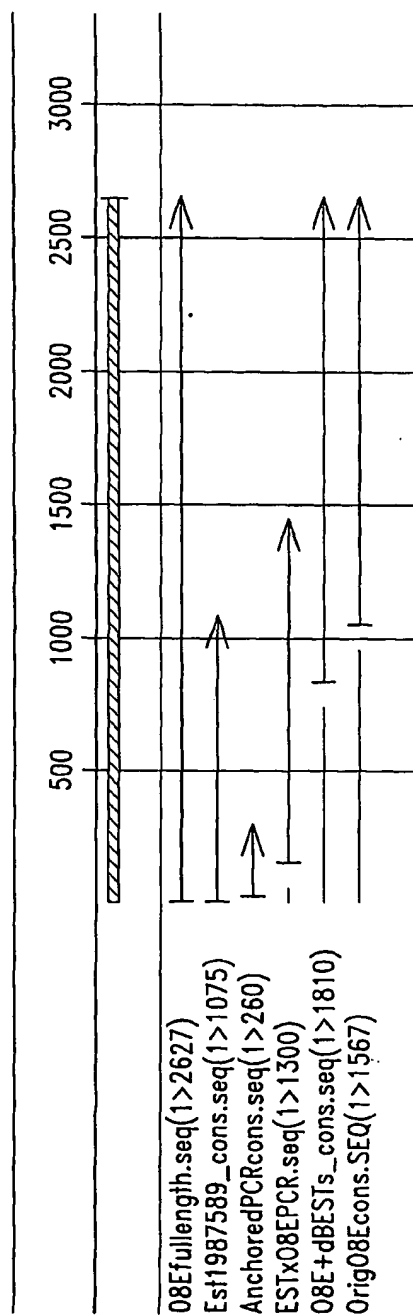


Fig. 16

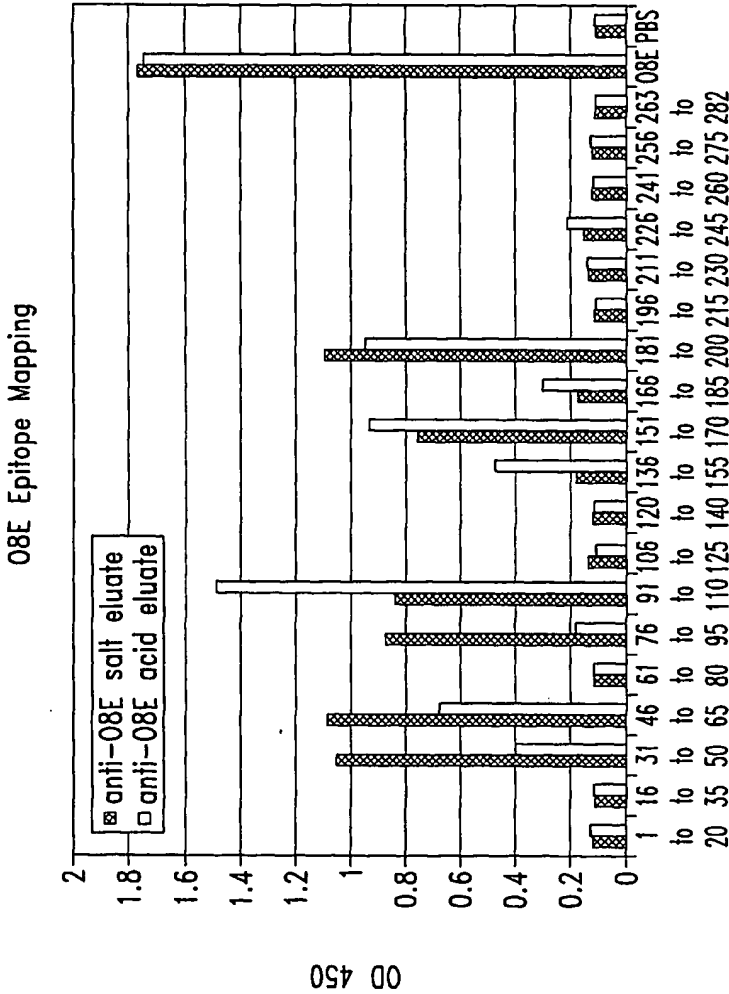
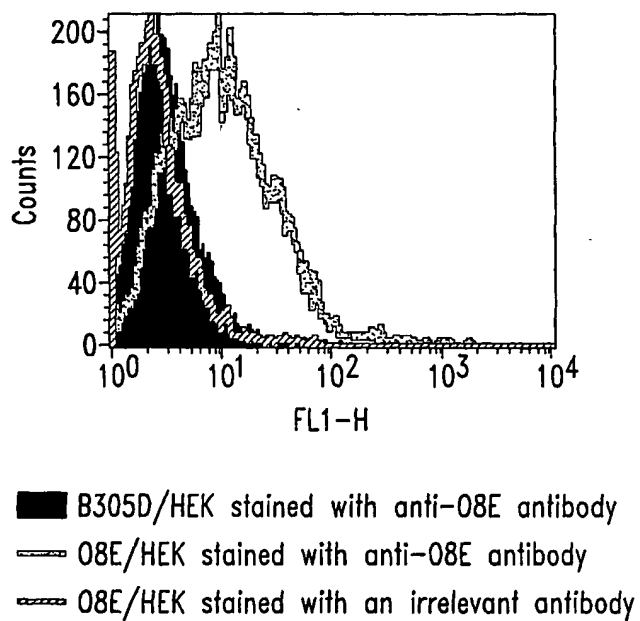


Fig. 17

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O8E Surface Expression

*Fig. 18*

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Surface expression of O8E

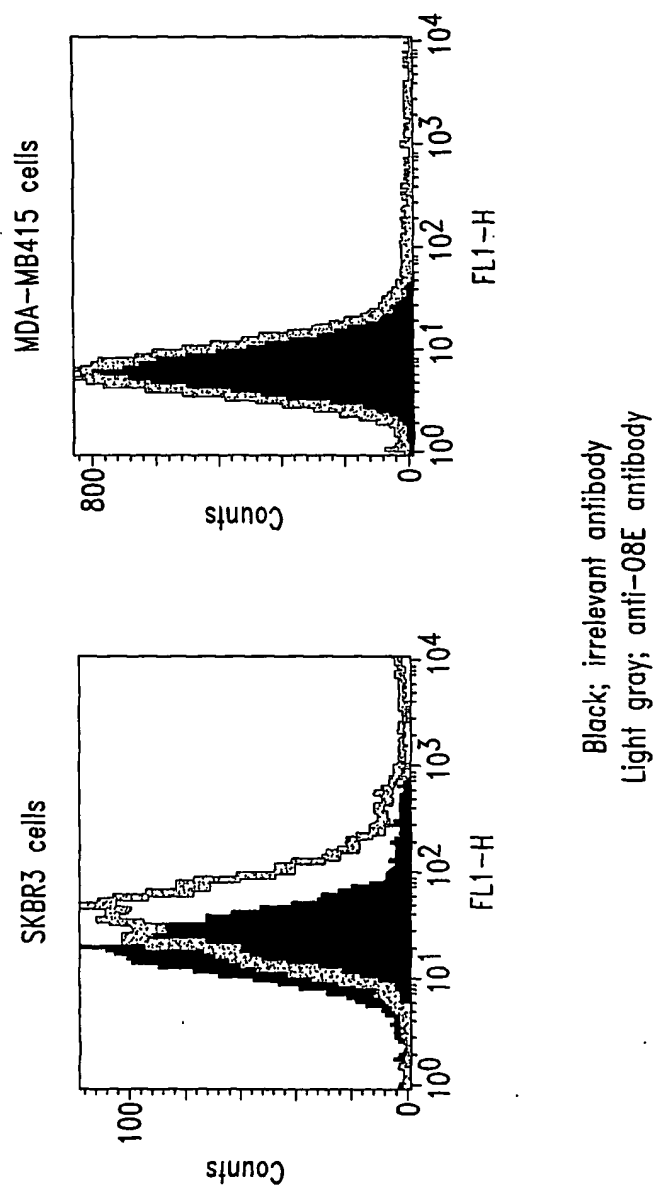
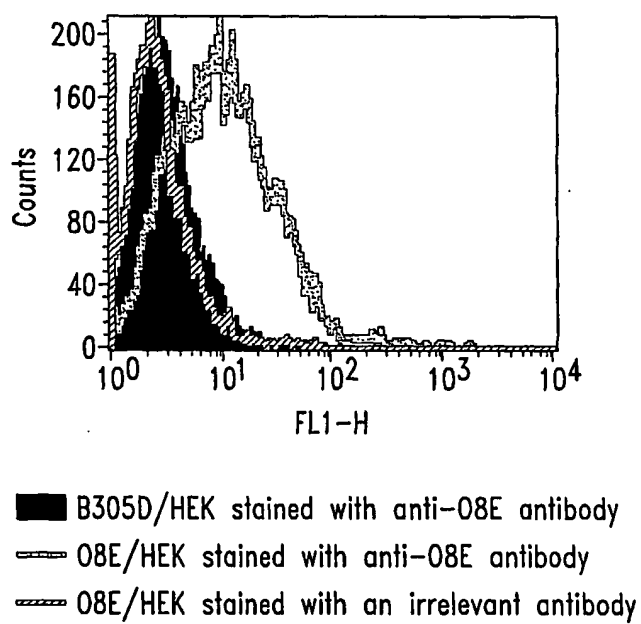


Fig. 19

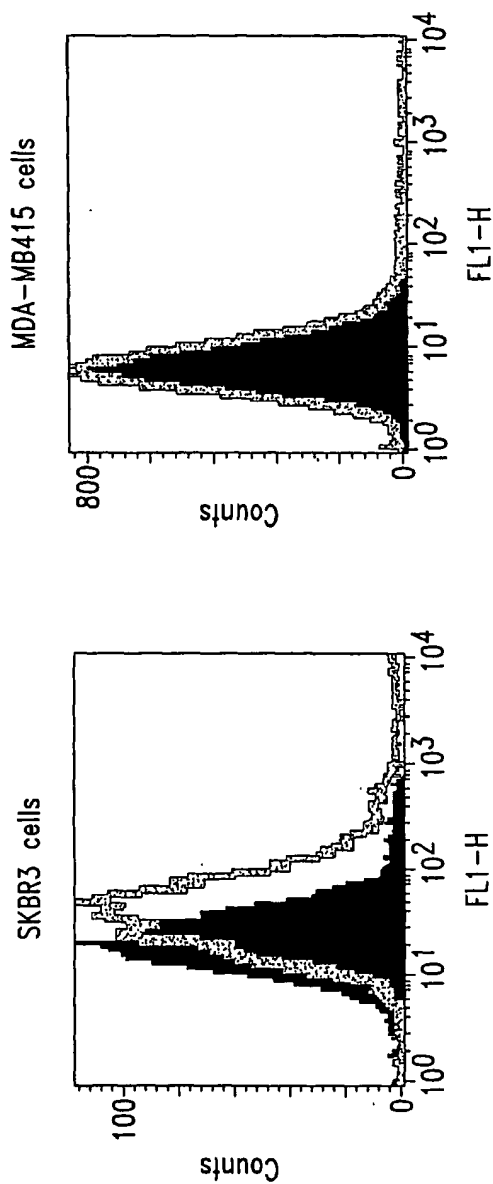
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O8E Surface Expression

*Fig. 20*

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Surface expression of O8E



Black; Irrelevant antibody
Light Grey; Anti-O8E antibody

Fig. 21

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O8E expression in HEK293 Cells
(probed with anti-O8E rabbit polyclonal sera #2333L)

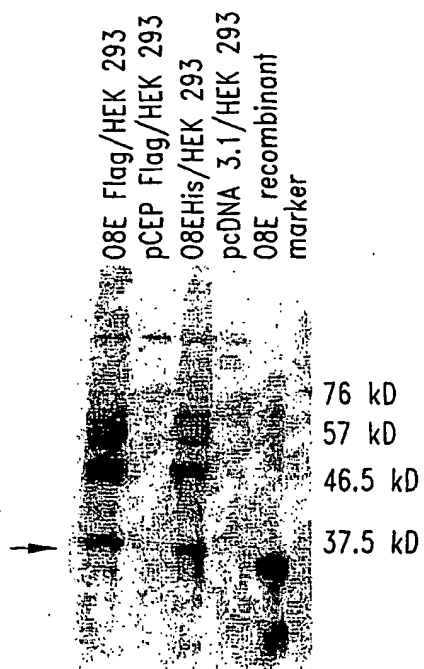


Fig. 22

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08E Rabbits 01212000

Date: 1/21/99

Antigen on Plate	Sera Sample	Antibody Dilutions											
		1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000
08E (#632-24)	Preimmune sera (#2576L):11/10/99	0.13	0.09	0.08	0.07	0.07	0.07	0.07	0.06	0.07	0.07	0.07	0.07
	Average	0.10	0.08	0.07	0.07	0.07	0.07	0.07	0.06	0.06	0.07	0.06	0.07
	α -08E (#2576K):1/11/2000	0.11	0.08	0.07	0.07	0.07	0.07	0.07	0.06	0.07	0.07	0.06	0.07
	Average	2.92	2.81	2.74	2.70	2.58	2.08	1.61	1.01	0.68	0.40	0.24	0.15
		2.93	2.77	2.74	2.69	2.48	2.08	1.57	1.00	0.66	0.40	0.23	0.16
	Average	2.93	2.79	2.74	2.69	2.53	2.08	1.59	1.00	0.67	0.40	0.23	0.16
	Preimmune sera (#2333L):11/10/99	0.09	0.07	0.06	0.06	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	Average	0.08	0.07	0.06	0.07	0.10	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	α -08E (#2333L):1/11/2000	0.08	0.07	0.06	0.06	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	Average	2.73	2.75	2.64	2.48	2.30	1.78	1.41	0.92	0.58	0.32	0.20	0.14
	Average	2.73	2.76	2.51	2.60	2.37	1.93	1.44	0.88	0.58	0.35	0.20	0.14
		2.73	2.76	2.57	2.54	2.33	1.85	1.43	0.90	0.58	0.33	0.20	0.14

Fig. 23

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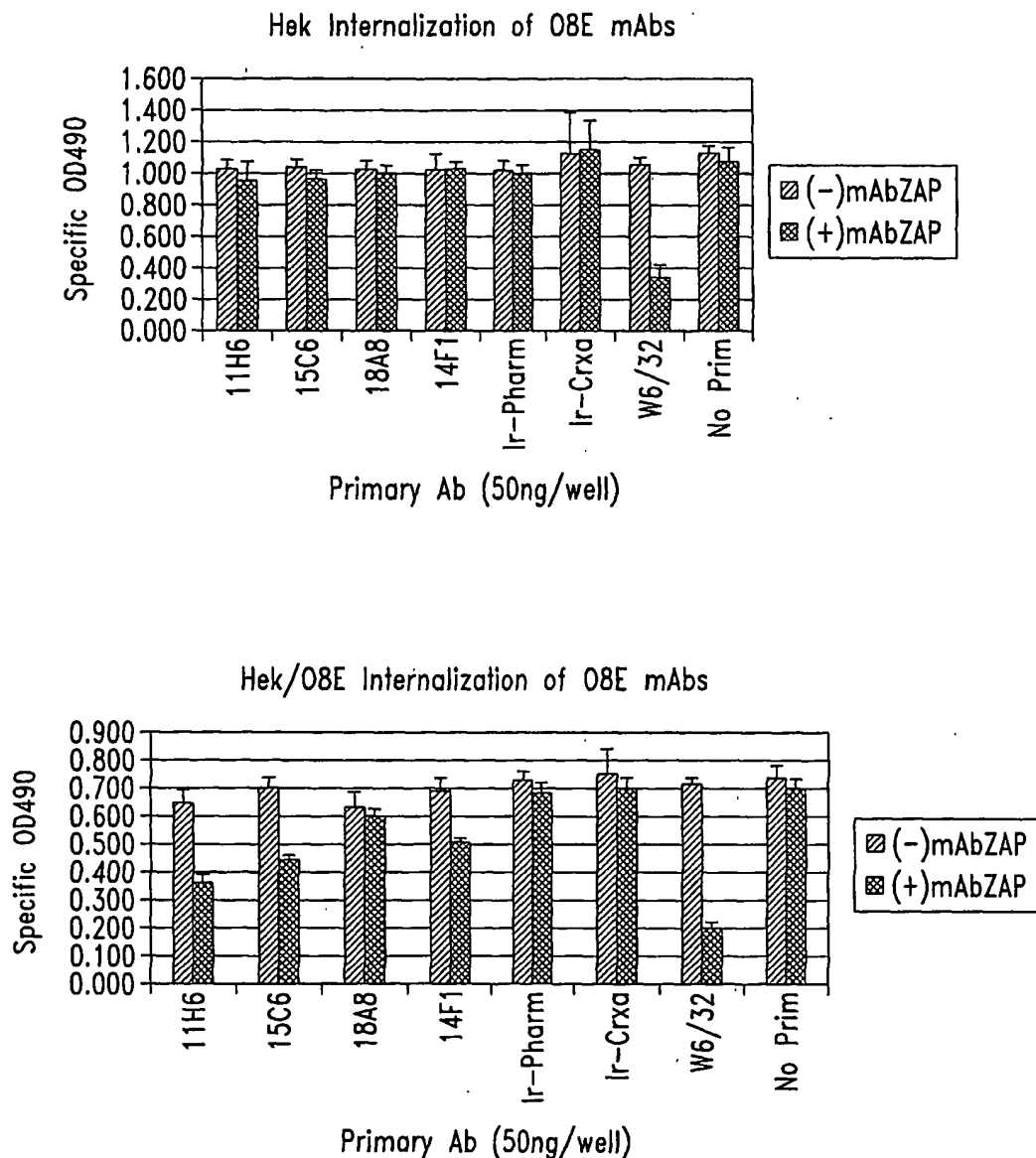
affi-pure O8E #2576L 739.87A&B

Date: 5/2/2000													
Antibody Name	O8E polyclonal												
Rabbit #, Bleed Date	2576L, 1/11/2000												
Purification Method	affinity												
Buffer	PBS												
Notebook	#705, p150												
lot #	739.87A	739.87B											
Antibody Concentration	1.4mg/ml	1.7mg/ml											
Initial Amount	18mg	3mg											
Antigen on Plate	Sera Sample	Antibody Dilutions											
O8E #632-24	preimmune sera (2576L)	1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000
		0.15	0.11	0.09	0.08	0.08	0.07	0.07	0.07	0.07	0.08	0.07	0.08
	Average	0.14	0.10	0.09	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	α -O8E (2576K):2/8/2000	0.14	0.10	0.09	0.08	0.07	0.07	0.07	0.07	0.07	0.08	0.07	0.08
		2.74	2.71	2.63	2.49	2.29	1.87	1.39	0.92	0.57	0.33	0.20	0.14
		2.72	2.68	2.64	2.47	2.26	1.93	1.42	0.94	0.57	0.34	0.21	0.14
	Average	2.73	2.70	2.63	2.48	2.27	1.90	1.41	0.93	0.57	0.34	0.21	0.14
	affinity pure α -O8E poly	2.69	2.60	2.50	2.21	1.83	1.34	0.99	0.64	0.38	0.22	0.15	0.11
	salt peak 739-87A	2.59	2.48	2.38	2.21	1.82	1.33	1.00	0.62	0.37	0.22	0.14	0.11
	Average	2.64	2.54	2.44	2.21	1.83	1.34	1.00	0.63	0.37	0.22	0.15	0.11
	affinity pure α -O8E poly	2.46	2.39	2.40	2.34	2.08	1.73	1.29	0.81	0.49	0.29	0.19	0.13
	acid peak 739-67B	2.65	2.66	2.61	2.45	2.14	1.76	1.30	0.82	0.48	0.29	0.19	0.13
	Average	2.56	2.53	2.51	2.39	2.11	1.74	1.30	0.81	0.49	0.29	0.19	0.13

Fig. 24

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Anti-O8E mAb Binding to O8E Amino Acids
61-80 Induces Ligand Internalization

*Fig. 25*

SEQUENCE LISTING

<110> Corixa Corporation
 Mitcham, Jennifer L.
 King, Gordon E.
 Algate, Paul A.
 Fling, Steven P.
 Retter, Marc W.
 Fanger, Gary Richard
 Reed, Steven G.
 Vedvick, Thomas S.
 Carter, Darrick
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 Albone, Earl

<120> COMPOSITIONS AND METHODS FOR THE THERAPY
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tagattttct gaatgcaaaa ataaaatgtg aactaatgaa ctttaggtta tacatattca 300
taaaataatt attcacatat ttcttgattt atcacagaaa taatgtatga aatgctttga 360
gtttcttgga gtaaactcca ttactcatcc caagaaacca tattataagt atcactgata 420
ataagaacaa caggaccttg tcataaattc tggataagag aaatagtctc tgggtgtttg 480
ntcttaattg ataaaattta cttgtccatc ttttagttca gaatcacaaa a 531

<210> 9

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 528

<223> n = A,T,C or G

<400> 9

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aagcggaaat gagaaaggag ggaaaatcat gtggtattga gcggaaaact gctggatgac 60
agggctcagt cctgttgag aactctgggt ggtgctgtag aacaggcca ctcacagtgg 120
ggtgcacaga ccagcacggc tctgtgacct gtttgttaca ggtccatgat gaggtaaaca 180
atacactgag tataagggtt ggtttagaaa ctcttacagc aatttgacaa agtaatcttc 240
tgtgcagtga atctaagaaa aaaattgggg ctgtatttgt atgttccttt ttttcatttc 300
atgttctgag ttacctatct ttattgcatt ttacaaaagc atccttccat gaaggaccgg 360
aagttaaaaa caaagcaggt cctttatcac agcactgtcg tagaacacag ttcagagtta 420
tccaccaag gagccaggga gctgggctaa accaaagaat ttgtcttttg gttaatcatc 480
aggtacttga gttggaattg ttttaatccc atcattacca ggctggangt g 531
```

<210> 10

<211> 861

<212> DNA

<213> Homo sapiens

<400> 10

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ccgcggctcc tgtccagacc ctgacctcc ctccaaggc tcaaccgtcc cccaacaacc 60
gccagccttg tactgatgtc ggctgcgaga gcctgtgctt aagtaagaat caggccttat 120
tggagacatt caagcaaagg ttggacaact acttttccag aacagaaagg aaactcatgc 180
atcagaaaag gtgactaata aaggtagcag aagaatatgg ctgcacaaat accagaatct 240
gatcagataa aacagtttaa ggaatttctg gggacctaca ataaacttac agagacctgc 300
tttttgact gtgttagaga cttcacaaca agagaagtaa aacctgaaga gaccacctgt 360
tcagaacatt gcttacagaa atatttaaaa atgacacaaa gaatatccat gagatttcag 420
gaatatcata ttcagcagaa tgaagccctg gcagccaaag caggactcct tggccaacca 480
cgatagagaa gtcctgatgg atgaactttt gatgaaagat tgccaacagc tgctttattg 540
gaaatgagga gtcactgat agaatcccct gaaagcagta gccaccatgt tcaaccatct 600
gtcatgactg tttggcaaat ggaaaccgct ggagaaacaa aattgctatt taccaggaat 660
aatcacaata gaaggctcta ttgttcagt aaataataag atgcaacatt tgttgaggcc 720
ttatgattca gcagcttggt cacttgatta gaaaaataaa ccattgtttc ttcaattgtg 780
actgttaatt ttaaagcaac ttatgtgttc gatcatgtat gagatagaaa aatttttatt 840
actcaaagta aaataaatg a 861
```

<210> 11

<211> 541

<212> DNA

<213> Homo sapiens

<400> 11

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gaaaaaaat ataaaacaca cttttgcgaa aacggtggcc ctaaaagagg aaaagaattt 60
caccaattata aatccaattt tatgaaaact gacaatttaa tccaagaatc acttttghta 120
atgaagctag caagtgatga tatgataaaa taaacgtgga ggaaataaaa acacaagact 180
tggcataaga tatatccact tttgatatta aacttgtgaa gcatattctt cgacaaattg 240
tgaaagcgtt cctgatcttg cttgttctcc atttcaaata aggaggcata tcacatccca 300
agagtaacag aaaaagaaaa aagacatttt tgcattttga gatgaaccaa agacacaaaa 360
caaacgaac aaagtgtcat gtctaattct agcctctgaa ataaaccttg aacatctcct 420
acaaggcacc gtgatttttg taattctaac ctgaagaaat gtgatgactt ttgtggacat 480
gaaaatcaga tgagaaaact gtggtctttc caaagcctga actcccctga aaaccttttg 540
a 541
```

<210> 12

<211> 541
<212> DNA
<213> Homo sapiens

<400> 12
ctgggatcat ttctcttgat gtcataaaag actcttcttc ttctctttca tctcttcttt 60
catcctcttc tgtacagtgc tgccgggtac aacggctatc tttgtcttta tctgagatg 120
aagatgatgc ttctgtttct cctaccataa ctgaagaaat ttcgctggaa gtcgtttgac 180
tggctgtttc tctgacttca ccttctttgt caaacctgag tctttttacc tcatgcccct 240
cagcttccac agcatcttca tctggatgtt tatttttcaa agggctcact gaggaaactt 300
ctgattcaga ggtcgaagag tcaactgtgat ttttctctc attttgctgc aaatttgcct 360
ctttgctgtc tgtgctctca ggcaacccat ttgttgctat gggggctgac aaagaaacct 420
ttggtcgatt aagtggcctg ggtgtcccag gccatttat attagacctc tcagtatagc 480
ttggtgaatt tccaggaaac ataacacatc tcattcgatt taaactattg gaattgggtt 540
t 541

<210> 13
<211> 441
<212> DNA
<213> Homo sapiens

<400> 13
gagggttggt ggtagcggct tggggaggtg ctgctctgt cggctcttgct ctctcgacg 60
cttcccccg ctcccttctg tcccccccc cggctgcctg cgtgccggag tgtgtgcgag 120
ggagggggag ggctgcggg ggggtggggg aggcgttccg gtccccaaga gaccgcgga 180
gggagggcga ggctgtgagg gactccggga agccatggac gtcgagaggc tccaggaggc 240
gctgaaagat tttgagaaga gggggaaaaa ggaagtgtt cctgtcctgg atcagtttct 300
ttgtcatgta gccaagactg gagaaacaat gattcagtgg tcccaattta aaggctattt 360
tattttcaaa ctggagaaag tgatggatga tttcagaact tcagctcctg agccaagagg 420
tcttccaac cctaattgtc a 441

<210> 14
<211> 131
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 126
<223> n = A,T,C or G

<400> 14
aagcaggcgg ctcccgcgct cgcagggcgg tgccacctgc ccgccgccg gctcgtcgc 60
tcgcccgccg cgccgcgctg ccgaccgcca gcatgctgcc gagagtgggc tgccccgcgc 120
tgccngtgcc g 131

<210> 15
<211> 692
<212> DNA
<213> Homo sapiens

<400> 15
atctcttgta tgccaaatat ttaatatata tctttgaaac aagttcagat gaaataaaaa 60
tcaaagtttg caaaaacgtg aagattaact taattgtcaa atattcctca ttgccccaaa 120
tcagtatttt ttttatttct atgcaaaagt atgccttcaa actgcttaaa tgatatatga 180
tatgatacac aaaccagttt tcaaatagta aagccagtca tcttgcaatt gtaagaaata 240
ggtaaaagat tataagacac cttacacaca cacacacaca cacacacgtg tgcacgccaa 300
tgacaaaaaa caatttggcc tctcctaaaa taagaacatg aagaccctta attgctgcc 360

```

ggaggggaaca ctgtgtcacc cctccctaca atccaggtag tttcctttaa tccaatagca 420
aatctgggca tatttgagag gagtgattct gacagccacg ttgaaatcct gtggggaacc 480
attcatgtcc acccactggg gccctgaaaa aatgccaaata atttttcgct cccacttctg 540
ctgctgtctc ttccacatcc tcacatagac cccagaccgg ctggcccctg gctgggcatc 600
gcattgctgg tagagcaagt cataggtctc gtctttgacg tcacagaagc gatacaccaa 660
attgcctggg cggtcattgt cataaccaga ga 692

```

```

<210> 16
<211> 728
<212> DNA
<213> Homo sapiens

```

```

<400> 16
cagacgggggt ttactatgt tggctaggct ggtcttgaac tcctgacttc aggtgatctg 60
cctgccttgg cctcccaaag tgctgggatt acaggcataa gccactgcgc ccggctgac 120
tgatggtttc ataaggcttt tccccctttt gtcagcact tctccttcct gccgccatgt 180
gaagaaggac atgtttgctt ccccttccac cacgattgta agttgtttcc tgaggcctcc 240
ccggccatgc tgaactgtga gtcaattaaa cctctttcct ttataaatta tccagttttg 300
ggtatgtctt tattagtaga atgagaacag actaatacaa cccttaaagg agactgacgg 360
agaggattct tcctggatcc cagcacttcc tctgaatgct actgacattc ttcttgagga 420
ctttaaactg ggagatagaa aacagattcc atggctcagc agcctgagag cagggaggga 480
gccaagctat agatgacatg ggcagcctcc cctgaggcca ggtgtggccg aacctgggca 540
gtgctgccac ccacccacc agggccaagt cctgtccttg gagagccaag cctcaatcac 600
tgctagcctc aagtgtcccc aagccacagt ggctaggggg actcagggaa cagttcccag 660
tctgccctac ttctcttacc tttacccttc atacctcaa agtagaccat gttcatgagg 720
tccaaagg 728

```

```

<210> 17
<211> 531
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 518, 528
<223> n = A,T,C or G

```

```

<400> 17
aagcgaggaa gccactgcgg ctctgggctg aaaagcgggc ccaggctcgg gaacagaggg 60
aacgcgaaga acaggagcgg aagctgcagg ctgaaaggga caagcgaatg cgagaggagc 120
agctggcccg ggaggctgaa gccgggctg aacgtgaggc cgaggcgagg agacgggagg 180
agcaggaggc tcgagagaag gcgcaggctg agcaggagga gcaggagcga ctgcagaagc 240
agaaagagga agccgaagcc cgggtccggg aagaagctga gcgccagcgc caggagcggg 300
aaaagcactt tcagaaggag gaacaggaga gacaagagcg aagaaagcgg ctggaggaga 360
taatgaagag gactcggaat tcagaagccg ccgaaaccaa gaagcaggat gcaaaggaga 420
ccgcagctaa caattccggc ccagaccctt gtgaaagctg tagagactcg gccctctggg 480
cttcagaaa ggattctatt gcagaaagga aggagctnng ccccccangg a 531

```

```

<210> 18
<211> 1041
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 544
<223> n = A,T,C or G

```

<400> 18

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ctctgtggaa aactgatgag gaatgaattt accattaccc atgtttctcat cccaagcaa 60
agtgtgggt ctgattactg caacacagag aacgaagaag aacttttcct catcacaggat 120
cagcagggcc tcatcacact gggctggatt cactctcacc ccacacagac cgcgtttctc 180
tccagtgtcg acctacacac tctgtgtctt taccagatga tgttgccaga gtcagtagcc 240
attgtttgct cccaagtt ccaggaaact ggattcttta aactaactga ccatggacta 300
gaggagattt cttcctgtcg ccagaaagga ttcatccac acagcaagga tccacctctg 360
ttctgtagct gcagccacgt gactgttgtg gacagagcag tgaccatcac agaccttca 420
tgagcgtttg agtccaacac cttccaagaa caacaaaacc atatcagtg actgtagccc 480
cttaatttaa gctttctaga aagctttgga agtttttgta gatagtagaa aggggggcat 540
cacntgagaa agagctgatt ttgtatttca ggtttgaaaa gaaataactg aacatatttt 600
ttaggcaagt cagaaagaga acatggtcac caaaaagcaa ctgtaactca gaaattaagt 660
tactcagaaa ttaagtagct cagaaattaa gaaagaatgg tataatgaac ccccatatac 720
ccttccttct ggattcacca attgttaaca tttttttcct ctcagctatc cttctaattt 780
ctctctaatt tcaatttggt tatatttacc tctgggctca ataaggcat ctgtgcagaa 840
atttggaagc catttagaaa atcttttgga ttttctgtg gtttatggca atatgaatgg 900
agcttattac tggggtgagg gacagcttac tccatttgac cagattgttt ggctaacaca 960
tcccgaagaa tgattttgtc aggaattatt gttatttaat aaatatttca ggatattttt 1020
cctctacaat aaagtaacaa t                                     1041

```

<210> 19

<211> 1043

<212> DNA

<213> Homo sapiens

<400> 19

```

ctctgtggaa aactgatgag gaatgaattt accattaccc atgtttctcat cccaagcaa 60
agtgtgggt ctgattactg caacacagag aacgaagaag aacttttcct catcacaggat 120
cagcagggcc tcatcacact gggctggatt cactctcacc ccacacagac cgcgtttctc 180
tccagtgtcg acctacacac tctgtgtctt taccagatga tgttgccaga gtcagtagcc 240
attgtttgct cccaagtt ccaggaaact ggattcttta aactaactga ccatggacta 300
gaggagattt cttcctgtcg ccagaaagga ttcatccac acagcaagga tccacctctg 360
ttctgtagct gcagccacgt gactgttgtg gacagagcag tgaccatcac agaccttca 420
tgagcgtttg agtccaacac cttccaagaa caacaaaacc atatcagtg actgtagccc 480
cttaatttaa gctttctaga aagctttgga agtttttgta gatagtagaa aggggggcat 540
cacctgagaa agagctgatt ttgtatttca ggtttgaaaa gaaataactg aacatatttt 600
ttaggcaagt cagaaagaga acatggtcac caaaaagcaa ctgtaactca gaaattaagt 660
tactcagaaa ttaagtagct cagaaattaa gaaagaatgg tataatgaac ccccatatac 720
ccttccttct ggattcacca attgttaaca tttttttcct ctcagctatc cttctaattt 780
ctctctaatt tcaatttggt tatatttacc tctgggctca ataaggcat ctgtgcagaa 840
atttggaagc catttagaaa atcttttgga ttttctgtg gtttatggca atatgaatgg 900
agcttattac tggggtgagg gacagcttac tccatttgac cagattgttt ggctaacaca 960
tcccgaagaa tgattttgtc aggaattatt gttatttaat aaatatttca ggatattttt 1020
cctctacaat aaagtaacaa tta                                     1043

```

<210> 20

<211> 448

<212> DNA

<213> Homo sapiens

<400> 20

```

ggacgacaag gccatggcga tatcggatcc gaattcaagc ctttggaatt aaataaacct 60
ggaacaggga aggtgaaagt tggagtgaga tgtcttccat atctatacct ttgtgcacag 120
ttgaatggga actggttggg ttagggcat cttagagttg attgatggaa aaagcagaca 180
ggaactggtg ggaggtcaag tggggaagtt ggtgaatgtg gaataactta cctttgtgct 240
ccacttaaac cagatgtgtt gcagctttcc tgacatgcaa ggatctactt taattccaca 300
ctctcattaa taaattgaat aaaagggaat gttttggcac ctgatataat ctgccaggct 360
atgtgacagt aggaaggaaat ggtttcccct aacaagcca atgcactggg ctgactttat 420

```

aaattatttta ataaaatgaa ctattatc

448

<210> 21

<211> 411

<212> DNA

<213> Homo sapiens

<400> 21

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ggcagtgaca ttcaccatca tgggaaccac cttccctttt cttcaggatt ctctgtagtg 60
gaagagagca cccagtgttg ggctgaaaac atctgaaagt agggagaaga acctaaaata 120
atcagtatct cagagggctc taagggtcca agaagtctca ctggacattt aagtgccaac 180
aaaggcatalc tttcggaatc gccaaagtcaa aactttctaa cttctgtctc tctcagagac 240
aagtggagact caagagtcta ctgctttagt ggcaactaca gaaaactggg gttacccaga 300
aaaacaggag caattagaaa tggttccaat atttcaaagc tccgcaaaca ggatgtgctt 360
tcctttgccc atttaggggt tcttctcttt cctttctctt tattaaccac t 411
```

<210> 22

<211> 896

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 230, 320

<223> n = A,T,C or G

<400> 22

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tgcgctgaaa acaacggcct cctttactgt taaaatgcag ccacaggtgc ttagccgtgg 60
gcatctcaac caccagcctc tgtggggggc aggtggggtt ccctgtgggc ctctggggcc 120
acgtccagcc tctgtcctct gccttccgtt cttcgacagt gtcccgga tccctgggtca 180
cttggtactt ggctggggcc tcctgtgctg ctccagcagc tcctccaggn ggctggggcc 240
cttcaccgca gcctcatgtt gtgtccggag gctgtcacg gcctcctcct tcctcgcgag 300
ggctgtcttc accctccggn gcacctcctc cagctccagc tgctggcggg cctgcagcgt 360
ggccagctcg gccctggcct gcgcggtctc ctcccarag gctgccagcc ggtcctcgaa 420
ctcctggcgg atcacctggg ccagggttgc gcgctcgcta gaaagctgct cgttcaccgc 480
ctgcgcaccc tcacagcggc gctccttctg ccgcacaagg ccctgcagac gcagattctc 540
gccctcgggc tccccaaagt ggcccttcag ctccgagcac cgctcctgaa gcttcgctc 600
cgactgctcc agctcggaga gctcggcctc gtacttgctc cgtaagcgct tgatgcggt 660
ctcggcagcc ttctcactct cctccttggc cagcgccatg tcggcctcca gccggtgaat 720
gaccagctca atctccttgc cccggccttt cgggatttct tccctcagct cctgttcccg 780
gttcagcagc cagcctcct ccttccgtgt cgggcgggcc tcccacgcct gcctctccag 840
ctccagctgc tgcttcaggg tattcagctc catctggcgg gcctgcagcg tggcca 896
```

<210> 23

<211> 111

<212> DNA

<213> Homo sapiens

<400> 23

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caacttatta cttgaaatta taatatagcc tgtccgtttg ctgtttccag gctgtgatat 60
attttcctag tggtttgact ttaaaaataa ataaggttta attttctccc c 111
```

<210> 24

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
 <222> 472, 494
 <223> n = A,T,C or G

<400> 24
 tgcaagtcac gggagtttat ttatttaatt tttttcccca gatggagact ctgtcgccca 60
 ggctggagtg caatgggttg atcttggtc actgcaacct ccacctcctg gggtcaagcg 120
 attctcctgc cacagcctcc cgagtagctg ggattacagg tgcccgccac cacaccagc 180
 taatttttat attttttagta aagacagggt ttcccatgt tggccaggct ggtcttgaac 240
 ttctgacctc aggtgatcca cctgcctcgg cctcccaaag tgttgggatt acaggcgtga 300
 gctaccctg cctggccagc cactggagtt taaaggacag tcatgttggc tccagcctaa 360
 ggcggcattt tccccatca gaaagccgc ggctcctgta cctcaaaata gggcacctgt 420
 aaagtcagtc agtgaagtct ctgctctaac tggccaccgc gggccattgg cntctgacac 480
 agccttgcca ggangcctgc atctgcaaaa gaaaagttca cttcctttcc g 531

<210> 25
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 377
 <223> n = A,T,C or G

<400> 25
 cagagaatct kagaaagatg tcgcgttttc ttttaatgaa tgagagaagc ccatttgtat 60
 ccctgaatca ttgagaaaag gcggcggttg cgacagcggc gacctaggga tcgatctgga 120
 gggacttggg gagcgtgcag agacctctag ctgcagcgcg agggacctcc cgccgggatg 180
 cctggggagc agatggaccc tactggaagt cagttggatt cagatttctc tcagcaagat 240
 actccttgcc tgataattga agattctcag cctgaaagcc aggttctaga ggatgattct 300
 ggttctcact tcagtatgct atctcgacac cttcctaata tccagacgca caaagaaaat 360
 cctgtgttgg atgttgngtc caatccttga acaaacagct ggagaagaac gaggagaccg 420
 gtaatatgtg gttcaatgaa catttgaaaag aaaaccagggt tgcagaccct g 471

<210> 26
 <211> 541
 <212> DNA
 <213> Homo sapiens

<400> 26
 gactgtcctg aacaagggac ctctgaccag agagctgcag gagatgcaga gtggtggcag 60
 gagtggaaagc caaagaacac ccaccttcct cccttgaagg agtagagcaa ccatcagaag 120
 atactgtttt attgctctgg tcaaacaagt cttcctgagt tgacaaaacc tcaggctctg 180
 gtgacttctg aatctgcagt ccactttcca taagttcttg tgcagacaac tgttcttttg 240
 cttccatagc agcaacagat gctttggggc taaaaggcat gtcctctgac cttgcagggtg 300
 gtggattttg ctcttttaca acatgtacat ccttactggg ctgtgctgtc acagggatgt 360
 ccttgctgga ctgttctgct atggggatat cttcgttgga ctgttcttca tgcttaattg 420
 cagtattagc atccacatca gacagcctgg tataaccaga gttggtggtt actgattgta 480
 gctgctcttt gtccacttca tatggcacia gtattttcct caacatcctg gctctgggaa 540
 g 541

<210> 27
 <211> 461
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> 367
 <223> n = A,T,C or G

<400> 27
 gaaatgtata tttaatcatt ctcttgaacg atcagaactc traaatcagt tttctataac 60
 arcatgtaat acagtcaccg tggtccaag gtccaggaag gcagtgggta acacatgaag 120
 agtgtgggaa gggggctgga aacaaagtat tcttttcctt caaagcttca ttcctcaagg 180
 cctcaattca agcagtcatt gtccttgctt tcaaaagtct gtgtgtgctt catggaagg 240
 atatgtttgt tgccttaatt tgaattgtgg ccaggaaggg tctggagatc taaattcaga 300
 gtaagaaaac ctgagctaga actcaggcat ttctcttaca gaacttggct tgcagggtag 360
 aatgaangga aagaaactta gaagctcaac aagctgaaga taatcccatc aggcatttcc 420
 cataggcctt gcaactctgt tcaactgagag atgttatcct g 461

<210> 28
 <211> 541
 <212> DNA
 <213> Homo sapiens

<400> 28
 agtctggagt gagcaaacaa gagcaagaaa caarragaag ccaaaagcag aaggctccaa 60
 tatgaacaag ataaatctat cttcaaagac atattagaag ttgggaaaat aattcatgtg 120
 aactagacaa gtgtgttaag agtgataagt aaaatgcacg tggagacaag tgcattccca 180
 gatctcaggg acctccccct gcctgtcacc tggggagtga gaggacagga tagtgcattg 240
 tctttgtctc tgaattttta gttatatgtg ctgtaatgtt gctctgagga agcccctgga 300
 aagctctatcc caacatatcc acatcttata ttccacaaat taagctgtag tatgtaccct 360
 aagacgctgc taattgactg ccacttcgca actcaggggc ggctgcattt tagtaatggg 420
 tcaaattgatt cactttttat gatgcttccc aagggtgcctt ggcttctctt cccaactgac 480
 aaatgcccaa gttgagaaaa atgatcataa ttttagcata aaccgagcaa tcggcgaccc 540
 c 541

<210> 29
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 29
 tagctgtctt cctcaactctt atggcaatga ccccatatct taatggatta agataatgaa 60
 agtgtatttc ttacactctg tatctatcac cagaagctga ggtgatagcc cgcttgtcat 120
 tgtcatccat attctgggac tcaggcggga actttctgga atattgccag ggagcatggc 180
 agaggggcac agtgcattct gggggaatgc acattggctc agcctgggta atgagtgata 240
 tacattacct ctgttcacaa ctcatgccc agcaccagtc acaaggcccc accaaatacc 300
 agagcccaag aaatgtagtc ctgttgatat ggttttgctg tgtcccaacc caaatctcat 360
 cttgaattgt aagctcccat aattcccatg tgttgtggga gggacctggt g 411

<210> 30
 <211> 511
 <212> DNA
 <213> Homo sapiens

<400> 30
 atcatgagga tgttaccaa gggatggtag taaaccattt gtattcgtct gttttcacac 60
 tgctttgaag atactacctg agactgggta atttataaac aaaagagatt taattgactc 120
 acagttctgc atggctgaag aggcctcagg aaacttacag tcatgggtga aggcaaaagg 180
 ggagcaaggc atgtcttaca tgtcagtagg agagagagcg agagcaggag aacctgccac 240
 ttataaacca ttcagatctc ataactccct atcatgagaa aaacatggag gaaaccaccc 300
 tcatgatcca atcacctccc gccaggctccc tccctcgaca cgtggggatt ataattcagg 360
 attagaggga cacagagaca aaccatatca tcattcatga gaaatccacc ctcatagtcc 420

aatcagctcc taccaggccc cacctccaac actggggatt gcaattcaac atgagatttg 480
 gatggggaca cagattcaaa ccatatcata c 511

<210> 31
 <211> 827
 <212> DNA
 <213> Homo sapiens

<400> 31
 catggccttt ctcccttagag gccagaggtg ctgccctggc tgggagtga gctccaggca 60
 ctaccagctt tcctgatttt cccgtttggt ccatgtgaag agctaccacg agccccagcc 120
 tcacagtgtc cactcaaggg cagcttgggc ctcttgctct gcagaggcag gctgggtgtga 180
 ccctgggaac ttgaccggg aacaacaggt ggcccagagt gagtgtggcc tggcccctca 240
 acctagtgtc cgctctctc tctcctggag ccagtcttga gtttaaaggc attaagtgtt 300
 agatacaagc tccttgtggc tggaaaaaca cccctctgct gataaagctc agggggcact 360
 gaggaagcag agggcccctt gggtgcccct cctgaagaga gcgtcaggcc atcagctctg 420
 tccctctggt gctcccacgt ctgttctctc ccctccatct ctgggagcag ctgcacctga 480
 ctggccacgc gggggcagtg gaggcacagg ctccagggtg ccgggctacc tggcacccta 540
 tggctttaca agtagagttg gccagtttc ctccacctg aggggagcac tctgactcct 600
 aacagtcttc cttgccctgc catcatctgg ggtggctggc tgtcaagaaa ggccgggcat 660
 gctttctaaa cacagccaca ggaggcttgt agggcatctt ccagggtggg aaacagtctt 720
 agataagtaa ggtgacttgc ctaaggcctc ccagcaccct tgatcttgga gtctcacagc 780
 agactgcatg tsaacaactg gaaccgaaaa catgcctcag tataaaa 827

<210> 32
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 32
 ccagaacctc cttctctttg gagaatgggg aggcctcttg gagacacaga gggtttcacc 60
 ttggatgacc tctagagaaa ttgcccaaga agcccacctt ctggtcccaa cctgcagacc 120
 ccacagcagt cagttgggtc ggccctgctg tagaaggcca cttggctcca ttgctgctt 180
 ccaaccaatg ggcaggagag aaggccttta tttctgccc acccattctc ctgtaccagc 240
 acctccgttt tcagtcagyg ttgtccagca acggtaccgt ttacacagtc a 291

<210> 33
 <211> 491
 <212> DNA
 <213> Homo sapiens

<400> 33
 tgcagttagt tttatttatg tgttttsgtc tggaaaacca agtgtcccag cagcatgact 60
 gaacatcact cacttcccct acttgatcta caaggccaac gccgagagcc cagaccagga 120
 ttccaaacac actgcacgag aatattgttg atccgctgtc aggttaagtgt ccgtcactga 180
 cccaracgct gttacgtggc acatgactgt acagtgccac gtaacagcac tgtacttttc 240
 toccatgaac agttacctgc catgtatcta catgattcag aacattttga acagttaatt 300
 ctgacacttg aataatccca tcaaaaaccg taaaatcact ttgatgtttg taacgacaac 360
 atagcatcac tttacgacag aatcatctgg aaaaacagaa caacgaatac atacatctta 420
 aaaaatgctg ggggtggcca ggcacagctt cagcctgta atcccagcac tttgggaggc 480
 ttaagcgggt g 491

<210> 34
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> 453, 476, 487
 <223> n = A,T,C or G

<400> 34
 tggggcggaa agaagccaag gccaaaggagc tgggtgcggca gctgcagctg gagggccgagg 60
 agcagaggaa gcagaagaag cggcagagtg tgtcgggcct gcacagatac cttcacttgc 120
 tggatggaaa tgaaaattac ccgtgtcttg tggatgcaga cggatgatgtg atttccttcc 180
 caccaataac caacagttag aagacaaagg ttaagaaaac gacttctgat ttgttttttg 240
 aagtaacaag tgccaccagt ctgcagattt gcaaggatgt catggatgcc ctcatctga 300
 aaatggcaag aaatgaaaaa gtacacttta gaaaataaag aggaaggatc actctcagat 360
 actgaagccg atgcagtctc tggacaactt ccagatccca caacgaatcc cagtgtgga 420
 aaggacgggc ccttccttct ggtggtggaa cangtcccgg tggatgatct tggaanggaa 480
 cctgaangtg gtgtaccccg tccaaggccg accttgcca c 521

<210> 35
 <211> 161
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 18
 <223> n = A,T,C or G

<400> 35
 tcccgcgctc gcagggcncg tgccacctgc cygtccgccc gctcgcctgc tcgcccgcgc 60
 cgccgcgctg ccgaccgyca gcatgctgcc gagagtgggc tgcccgcgc tgccgctgcc 120
 gccgcccgcg ctgctgccgc tgctgccgct gctgctgctg c 161

<210> 36
 <211> 341
 <212> DNA
 <213> Homo sapiens

<400> 36
 ggcggttagg catggaactg agaagaacga agaagctttc agactacgtg gggaagaatg 60
 aaaaaaccaa aattatcgcc aagattcagc aaaggggaca gggagctcca gcccgagagc 120
 ctattattag cagtgaggag cagaagcagc tgatgctgta ctatcacaga agacaagagg 180
 agctcaagag attggaagaa aatgatgatg atgcctattt aaactcacca tgggcggata 240
 aactgcttt gaaaagacat ttcatggag tgaaagacat aaagtggaga ccaagatgaa 300
 gttcaccagc tgatgacact tccaaagaga ttagctcacc t 341

<210> 37
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 516
 <223> n = A,T,C or G

<400> 37
 tctgaagggtt aaatgtttca tctaaatagg gataatgrta aacacctata gcatagagtt 60
 gtttgagatt aaatgagata atacatgtaa aattatgtgc ctggcataca gcaagattgt 120
 tggtgtgtgt gatgatgatg atgatgatga taatatTTTT ctatccccag tgcacaactg 180
 cttgaacctt ttagataatc aatacatgtt tcttgaactg agatcaattt ccccatgttg 240

```

tctgactgat gaagccctac attttcttct agaggagatg acatttgagc aagatcttaa 300
agaaaatcag atgccttcac ctgaccactg cttggtgatc ccatggcact ttgtacatct 360
ctccattagc tctcatctca ccagcccatc attattgtat gtgctgcctt ctgaagcttg 420
cagctggcta ccacmggta gaataaaaat catcctttca taaaatagtg accctccttt 480
tttatttgca tttcccaaag ccaagcaccg tggganggta g 521

```

<210> 38

<211> 461

<212> DNA

<213> Homo sapiens

<400> 38

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tatgaagaag ggaaaagaag ataatttgtg aaagaaatgg gtccagttac tagtctttga 60
aaagggtcag tctgtagctc ttcttaatga gaataggcag ctttcagttg ctcagggtca 120
gatttcctta gtggtgtatc taatcacagg aaacatctgt ggttccctcc agtctctttc 180
tgggggactt gggcccactt ctcatctcat ttaattagag gaaatagaac tcaaagtaca 240
atttactgtt gtttaacaat gccacaaaga catggttggg agctatttct tgatttgtgt 300
aaaatgctgt ttttgtgtgc tcataatggg tccaaaaaatt ggggtgctggc caaagagaga 360
tactgtttaca gaagccagca agaagacctc tgttcattca ccccccggg gatatcagga 420
attgactcca gtgtgtgcaa atccagtttg gcctatcttc t 461

```

<210> 39

<211> 769

<212> DNA

<213> Homo sapiens

<400> 39

```

tgagggactg attggtttgc tctctgctat tcaattcccc aagcccactt gttcctgcag 60
cgtcctcctt ctcatccctt ttagttgtac cctctctttc atctgagacc ttctcttctt 120
gatgtgcctt tttcttcttc ttgctttttc tgatgttctg ctcagcatgt tctgggtgct 180
tctcatctgc atcatccctt tcagatgctg tagcttcttc ctctctttc tgctcctttt 240
tctttttctt ttttttgggg ggcttgctct ctgactgcag ttgagggggc ccagggtcct 300
ggcctttgag acgagccagg aaggcctgct cctgggcctc taggcgagca agcttggcct 360
tcattgtgat cccaagacgg gcagccttgt gtgctgttcg cccctcacag gcttggagca 420
gcatctcatc agtcagaatc tttggggact tggaccctg gttgtogtca tcaactgcagc 480
tctccaagtc tttgtttggc ttctctccac ctgaagtcaa ttagccatc ttcacaaact 540
tctgatacag caagttgggc ttgggatgat tataacgggt ggtctcctta gaaaggctcc 600
ttatctgtac tccatcctgc ccagtttcca ctaccaagtt ggccgcagtc ttggtgaaga 660
gtcattcca ccagtgggtt gtgaactcct tggcagggtc atgtcctacc ccatgagtgt 720
cttgcttcag ygtcaccctg agagcctgag tgataccatt ctcttccg 769

```

<210> 40

<211> 292

<212> DNA

<213> Homo sapiens

<400> 40

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gacaacatga aataaatcct agaggacaaa attaaactca atagagtgtg gtctagttaa 60
aaactcgaag aatgagcaag tctggtggga gtggaggaag ggctatacta taaatccaag 120
tgggcctcct gatcttaaca agccatgctc attatacaca tctctgaact ggacatacca 180
cctttacgca ggaaacaggg cttggaactt ctaagggaag ttaacatgca ccaccacat 240
ctaaccctacc tgccgggtag gtaccatccc tgcttcgctg aaatcagtg c 292

```

<210> 41

<211> 406

<212> DNA

<213> Homo sapiens

<400> 41
 ttggaattaa ataaacctgg aacagggaag gtgaaagttg gagtgagatg tcttccatat 60
 ctataccttt gtgcacagtt gaatgggaac tgtttggtt tagggcatct tagagttgat 120
 tgatggaaaa agcagacagg aactggtggg aggtcaagtg gggaagttgg tgaatgtgga 180
 ataacttacc tttgtgctcc acttaaacca gatgtgttgc agctttcctg acatgcaagg 240
 atctacttta attccacact ctcattaata aattgaataa aagggaatgt tttggcacct 300
 gatataatct gccaggctat gtgacagtag gaaggaatgg tttcccctaa caagcccaat 360
 gcactggtct gactttataa attatttaat aaaatgaact attatc 406

<210> 42
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 42
 aaactggacc tgcaacaggg acatgaatth actgcarggt ctgagcaagc tcagcccctc 60
 tacctcaggg cccacagacc atgactacct ccccaggag cgggaggtg aagggggcct 120
 gtctctgcaa gtggagccag agtgaggaa tgagctctga agacacagca cccagccttc 180
 tcgcaccagc caagccttaa ctgcctgcct gaccctgaac cagaaccag ctgaactgcc 240
 cctccaaggg acaggaaggc tgggggaggg agtttacaac ccaagccatt ccaccccctc 300
 ccctgctggg gagaatgaca catcaagctg ctaacaattg ggggaagggg aaggaagaaa 360
 actctgaaaa caaatcttg t 381

<210> 43
 <211> 451
 <212> DNA
 <213> Homo sapiens

<400> 43
 catgcgtttc accactgttg gccaggctgg tctcgaactc ctggcctcaa gcaatccacc 60
 cgcctcagcc tccaaaagtg ctgggattac agatgtgagc catggcacca tgccaaaagg 120
 ctatattcct ggctctgtgt ttccgagact gcttttaatc ccaacttctc tacatttaga 180
 ttaaaaaata ttttattcat ggtcaatctg gaacataatt actgcatctt aagtttccac 240
 tgatgtatat agaaggctaa aggcacaatt ttatcaaat ctagtagagt aaccaaacat 300
 aaaatcatta attactttca acttaataac taattgacat tcctcaaaag agctgttttc 360
 aatcctgata gggtctttat tttttcaaaa tatatttgcc atgggatgct aatttgcaat 420
 aaggcgcata atgagaatac cccaaactgg a 451

<210> 44
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 44
 gttggacccc cagggactgg aaagacactt cttgcccag ctgtggcggg agaagctgat 60
 gttccttttt attatgcttc tggatccgaa tttgatgaga tgtttggtgg tgtgggagcc 120
 agccgtatca gaaatctttt tagggaagca aaggcgaatg ctccttgtgt tatatttatt 180
 gatgaattag attctgttgg tgggaagaga attgaatctc caatgcatcc atattcaagg 240
 cagaccataa attcaacttct tgctgaaatg gatggtttta aacccaatga aggagttatc 300
 ataataggag ccacaaactt cccagaggca ttagataatg ccttaataacc gtcctggctg 360
 ttttgacatg caagttacag ttccaaggcc agatgtaaaa ggtcgaacag aaattttgaa 420
 atgggtatctc aataaaaata agtttgatca atcccgttga tccagaaatt atagcctcga 480
 ggtactggtg gcttttccgg aagcagagtt gggagaatct t 521

<210> 45
 <211> 585
 <212> DNA
 <213> Homo sapiens

```

<400> 45
gcctacaaca tccagaaaga gtctaccctg cacctgggtgc tscgtctcag aggtgggatg 60
cagatcttcg tgaagaccct gactggtaag accatcactc tcgaagtgga gccgagtga 120
accatygaga acgtcaaagc aaagatccar gacaagggaag gcrtycctcc tgaccagcag 180
aggttgatct ttgccggaag gcagctggaa gatggdcgca ccctgtctga ctacaacatc 240
cagaaagagt cyaccctgca cctgggtgctc cgtctcagag gtgggatgca ratcttcgtg 300
aagaccctga ctggtaagac catcaccctc gaggtggagc ccagtgcacac catcgagaat 360
gtcaaggcaa agatccaaga taagggaaggc atccctcctg atcagcagag gttgatcttt 420
gctgggaaac agctggaaga tggacgcacc ctgtctgact acaacatcca gaaagagtcc 480
actctgcact tggctctgag cttgaggggg ggtgtctaag tttcccttt taaggtttcm 540
acaaatttca ttgcactttc ctttcaataa agttggttga tccc 585

```

```

<210> 46
<211> 481
<212> DNA
<213> Homo sapiens

```

```

<400> 46
gaactgggcc ctgagcccaa gtcattgcctt gtgtccgcat ctgccgtgtc acctctgtkc 60
ctgcccctca cccctccctc ctggtcttct gagccagcac catctccaaa tagcctattc 120
cttctctcaa atcacacaca catgcgggcc acacatacct gctgccctgg agatggggaa 180
gtaggagaga tgaatagagg ccatacatt gtacagaagg aggggcaggt gcagataaaa 240
gcagcagacc cagcggcagc tgaggtgcat ggagcacggt tggggccggc attgggctga 300
gcacctgatg ggcctcatct cgtgaatcct cgaggcagcg ccacagcaga ggagttaagt 360
ggcacctggg ccgagcagag caggagactg agggtcagag tggaggctaa gctgccctgg 420
aaactcctcaa tcttgccctgc cccctagtat gaagccccc tctgccccct acaattcctg 480
a 481

```

```

<210> 47
<211> 461
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 128
<223> n = A,T,C or G

```

```

<400> 47
atggatctta ctttgccacc cagggttgag tgcaagtgtg caatcttggc tcaactgcagc 60
cttaacctcc caggctcaag ctatcctcct gccaaagcct tccacatagc tgggactaca 120
ggtacacngc caccacaccc agctaaaatt tttgtatttt ttgtagagac gggatctcgc 180
cacgttgccc aggttggtcc catcctgacc tcaagcagat ctgccacact cagcccccca 240
acgtgtctagg attacaggcg tgagccaccg caccagcct ttgttttgct tttaatggaa 300
tcaccagttc ccctccgtgt ctcagcagca gctgtgagaa atgctttgca tctgtgacct 360
ttatgaaggg gaacttccat gctgaatgag ggtaggatta catgctcctg tttcccgggg 420
gtcaagaaaag cctcagactc cagcatgata agcagggtga g 461

```

```

<210> 48
<211> 571
<212> DNA
<213> Homo sapiens

```

```

<400> 48
ataggggctt taaggaggga attcagggtc aatgagggtc taaggccagg gctcttatcc 60
agtaagactg gggctccttag atgagaaaga gacacccgag gtccttctct ctgccgtgtg 120
aggatgcata aagaaggcgg ccgtctgcaa gcgaaggaga ggccgcacca gaaaccgaca 180

```

```

ccttcacatcct ggacttgacg cctctagaac tgagaaaata actgtctgtt ggtaaagcca 240
cccagtttgt agtattctct tatggcttcc taagcagact aacaaacaaa caccacaaat 300
taactgatgg ctctgctgtc ttctgtaaaa attgctatga gagaactttt cactcactgt 360
tttgacgttt ctccctcagt ccctgggtct ttcttctcac ataatcccaa tttcaattta 420
tagttcatgg ccaggcaga gtcattcatc acggcatctc ctgagctaaa ccagcacctg 480
ctctgctcac ttcttgactg gctgctcatc atcagccctc ttgcagagat ttcatttcct 540
cccgtgccag gtacttcacg caccaagctc a

```

<210> 49

<211> 511

<212> DNA

<213> Homo sapiens

<400> 49

```

ggataatgaa gttgttttat ttagcttgga caaaaaggca tttcctcta ttttcttata 60
caacaaatat ccccaaaata aagcaagcat atatatcttg aatgtgtaat aatccagtga 120
taaacaagag cagtacttta aaagaaaaaa aaatatgtat ttctgtcagg ttaaaatgag 180
aatcaaaacc atttactctg ctaactcatt attttttggc ttctttttgg ttaagagagg 240
caatgcaata cactgaaaaa ggtttttatc ttatctggca ttggaattag acatattcaa 300
accccagccc ccatttccaa actttaagac cacaacaag taatttactt ttctgaacat 360
tggttttttc tggaaaatgg gaattataaa atagactttg cagactctta tgagattaaa 420
taagataatg tatgaaattc tttcttcttt tttacttctt tttccttttt gagatggagt 480
ctcaccccggt caccagggt ggagtacagt g

```

<210> 50

<211> 561

<212> DNA

<213> Homo sapiens

<400> 50

```

ccactgcact ccagcctggg tgacggagtg agactctgtc tcaaaaaaac aaacaaacaa 60
acaaacaaaa aactgaaaag gaaatagagt tcctctttcc tcatatatga atatattatt 120
tcaacagatt gttgatcacc taccatatgc ttggtattgt tctaattgct ggggatacag 180
caagagggtc tgcagaactt catggagcat gaaagtaaat aaacaaagtt aatttcaagg 240
ccaggcatgg ttgctcacac cttagtccc agcactttgg gaggtgagg cagggtggatc 300
acttgggccc aggagttcaa ggctgcagt agccaagatt gtgccactac tctccagggt 360
gggcaacaga gcaagaccct gtctcagggg gaacaaaaag ttaatttcag attttgtaa 420
gtgctgtaaa ggaagtaaat aggttgatat tcaagagagc acctgaaggc caggcgtgg 480
ggctcacgcc tgtggtctaa cgctttggga agcccgagcg ggcggatcac aaggtcagga 540
gaattttggc caggcatggt g

```

<210> 51

<211> 451

<212> DNA

<213> Homo sapiens

<400> 51

```

agaatccatt tattgggttt taaactagtt acacaactga aatcagtttg gcactacttt 60
atacagggat tacgcctgtg tatgccgaca cttaataact gtaccaggac cactgctgtg 120
cttaggtctg tattcagtca ttcagcatgt agatactaaa aatatactgt agtggtcctt 180
taaggaagac tgtacagggt gtgttgcaag atgacattca ccaatttggt aattatttca 240
accagaaga tacctttcac tctataaact tgtcataggc aaacatgtgg tgtagcatt 300
gagagatgca cacaaaaatg ttacataaaa gttcagacat tctaatagata agtgaactga 360
aaaaaaaaaa aacccacat ctcaattttt gtaacaagat aaagaaaata atttaaaaac 420
acaaaaaatg gcattcagt ggtacaaagc c

```

<210> 52

<211> 682

<212> DNA

<213> Homo sapiens

<400> 52

```
caaatatttta atataaatct ttgaaacaag ttcagakgaa ataaaaatca aagtttgcaa 60
aaacgtgaag attaacttaa ttgtcaaata ttcctcattg ccccaaata gtatTTTTTT 120
tatttctatg caaaagtatg ccttcaaact gcttaaata tatatgatat gatacacaaa 180
ccagttttca aatagtaaag ccagtcattt tgcaattgta agaaataggt aaaagattat 240
aagacacctt acacacacac acacacacac acacacacgt gtgcaccgcc aatgacaaaa 300
aacaatttgg cctctcctaa aataagaaca tgaagaccct taattgctgc caggagggaa 360
cactgtgtca cccctcccta caatccaggt agtttccttt aatccaatag caaatctggg 420
catatttgag aggagtgatt ctgacagcca csgttgaaat cctgtgggga accattcatg 480
tccaccactt ggtgccctga aaaaatgcc aataattttt gctccactt ctgctgctgt 540
ctctccaca tcctcacata gacccagac ccgctggccc ctggtgggc atcgcttgc 600
tggtagagca agtcattaggt ctgctctttg acgtcacaga agcgatacac caaattgcct 660
ggtcgggtcat tgtcataacc ag                                     682
```

<210> 53

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 208

<223> n = A,T,C or G

<400> 53

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tttgacttta gtaggggtct gaactatttta ttttactttg ccmgtaatat ttaraccyta 60
tatatctttc attatgccat ctatctttct aatgbcaagg gaacagwtgc taamctggct 120
tctgcattwa tcacattaaa aatggctttc ttggaaaatc ttcttgatat gaataaagga 180
tcttttavag ccatcattta aagcmgntt ctctccaaca cgagtctgct sasgggggk 240
gagctgtgaa ctctggctga aggctttccc atacacactg caatgacmtg gtttctgacc 300
agbgtgagtt a                                     311
```

<210> 54

<211> 561

<212> DNA

<213> Homo sapiens

<400> 54

```
agagaagccc cataaatgca atcagtgtgg gaaggccttc agtcagagct caagcctttt 60
cctccatcat cggtttcata ctggagagaa accctatgta tgtaatgaat gcggcagagc 120
cttttggttt aactctcatc ttactgaaca cgtaaggatt cacacaggag aaaaacccta 180
tgtttgtaat gagtgcggca aagcctttcg tcggagtcc actcttgctc agcatcgaag 240
agttcacact ggggagaagc cctaccagtg cgttgaaatg gggaaagctt tcagccagag 300
ctcccagctc accctacatc agccgagttc acactggaga gaagccctat gactgtggtg 360
actgtgggaa ggccttcagc cggaggtcaa cctcattca gcatcagaaa gttcacagcg 420
gagagactcg taagtgcaga aaacatggtc cagcctttgt tcatggctcc agcctcacag 480
cagatggaca gattccact ggagagaagc acggcagaac cttaaccat ggtgcaaatc 540
tcattctgcg ctggacagtt c                                     561
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<210> 55

<211> 811

<212> DNA

<213> Homo sapiens

<400> 55

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gagacaggggt ctcactttgt caccagggct ggaatgcagt ggtgcgatct tacgtagctc 60
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ggactgtggg tgcatgccac catgcctggc taacttttgt agtttttgta aagatggggg 180
tttgccatgt tgcacatgct ggtcttgaac tcctgagctc aaacgatctg ccacacctcg 240
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atttttacta ggctttggat atttttttcc tttttcagct ttatacagag gattggatct 420
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gaggtgcagg ataaaggcct ttagtctgct ttgcacttt ttcttccact tttttgtaaa 600
cctgttgctt gacaaatgga attgacagcg tatgccatga ctattccatt tgtcaggcat 660
acgctgtcaa tttttccacc aatcccttgt ctctctttgg agagatcttc ttatcagcta 720
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gaaccctgga gaccaggact aaaacctcca g
811

```

<210> 56

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 45, 477, 490, 561

<223> n = A,T,C or G

<400> 56

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acaaaactag ggggctctgt cttctcatatc atcatacaat tttcaagtat tttttttatg 180
tacaaagagc tactctatct gaaaaaaaaat taaaaaataa atgagacaag atagttttatg 240
catcctagga agaaagaatg ggaagaaaga acggggcagt tgggtacaga ttctgtctcc 300
ctgttcccga ggaccactac cttcctgcca ctgagttccc ccacagcctc acccatcatg 360
tcacagggca agtgccaggg taggtgggga ccagtggaga caggaaccag caacatactt 420
tggcctggaa gataaggaga aagtctcaga aacacactgg tgggaagcaa tccccacnggc 480
cgtgccccan gagcttccca cctgctgctg gctccctggg tggctttggg aacagcttgg 540
gcaggccctt ttgggtgggg nccaactggg ctttggggcc cgtgtggaaa g
591

```

<210> 57

<211> 481

<212> DNA

<213> Homo sapiens

<400> 57

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aaacattgag atggaatgat agggtttccc agaatcaggt ccatatttta actaaatgaa 60
aattatgatt tatagccttc tcaaatacct gccatacttg atatctcaac cagagctaata 120
tttacctctt tacaaattaa ataagcaagt aactggatcc acaatttata atacctgtca 180
attttttctg tattaaacct ctatcatagt ttaagcctat tagggacttt aatccttaca 240
aataaacagg tttaaaatca cctcaatagg caactgccct tctggttttc ttctttgact 300
aaacaatctg aatgcttaag attttccact ttgggtgcta gcagtacaca gtgttacact 360
ctgtattcca gacttcttaa attatagaaa aagggaatgta cactttttgt attctttctg 420
agcaggggccg ggaggcaaca tcacttacca tggtagggac ttgtatgcat ggactacttt 480
a
481

```

<210> 58

<211> 141

<212> DNA

<213> Homo sapiens

<400> 58
 actctgtcgc ccaggctgga gccabtggm gcgatctcga ctccctgcaa gctmcgcctc 60
 acaggwtcat gccattctcc tgcctcagca tctggagtag ctgggactac aggcgccagc 120
 caccatgccc agctaatttt t 141

<210> 59
 <211> 191
 <212> DNA
 <213> Homo sapiens

<400> 59
 accttaaaga cataggagaa tttatactgg gagagaaagc ttacaaatgt aagggtttctg 60
 acaagacttg ggagtgattc acacctggaa caacatactg gacttcacac tggabagaaa 120
 ccttacaagt gtaatgagtg tggcaaagcc tttggcaagc agtcaacact tattcaccat 180
 caggcaattc a 191

<210> 60
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 60
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 aggttacata acagggtgac aagcccgtac ttttttcccta cagtcaggtc tgccggcccc 180
 gggttttagct gaaatatggg ccttatcaga tctgaacaag gatgggaaga tggaccagca 240
 agagttctct atagctatga aactcatcaa gttaaagttg cagggccaac agctgcctgt 300
 agtcctccct cctatcatga aacaaccccc tatgttctct ccactaatct ctgctcgttt 360
 tgggatggga agcatgccc atctgtccat tcatcagcca ttgcctccag ttgcacctat 420
 agcaacaccc ttgtcttctg ctacttcagg gaccagtatt cctccctaata gatgcctgct 480

<210> 61
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 61
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 tgtgtattat agctttctct gagttccttc agctgattgt taaatgaatc catttctgag 120
 agcttagatg cagtttcttt ttcaagagca tctaattgtt ctttaagtct ttggcataat 180
 tcttcctttt ctgatgactt tctatgaagt aaactgatcc ctgaatcagg tgtgttactg 240
 agctgcatgt ttttaattct ttctgtttaat agctgcttct cagggaccag atagataagc 300
 ttattttgat attccttaag ctcttgggtga agttgttcga tttccataat ttccagggtca 360
 cactgggttat cccaaacttc t 381

<210> 62
 <211> 906
 <212> DNA
 <213> Homo sapiens

<400> 62
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 tgaggcacct aggcgcgggc accccggcga caggaagccg tcctgaaccg ggctaccggg 120
 taggggaagg gccgcgtag tcctcgtagg gccccagagc tggagtcggc tccacagccc 180
 cgggcccgtcg gcttctcact tcctggacct ccccgccgcc cgggcctgag gactggctcg 240
 gcggaggagg aagaggaaac agacttgagc agctccccgt tgtctcgcaa ctccactgcc 300
 gaggaactct catttcttcc ctgcctcctt cccccccac ctcatgtaga aaggtgctga 360

```

agcgtccgga gggaagaaga acctgggcta ccgtcctggc cttcccmccc ctttcccggg 420
gcgcttttgt gggcgtggag ttggggttgg gggggtgggt gggggttctt ttttgagtg 480
ctggggaact tttttccctt cttcaggtca ggggaaaggg aatgcccaat tcagagagac 540
atgggggcaa gaaggacggg agtggaggag cttctggaac ttgagccg tcacgggag 600
gcggcagctc taacagcaga gacgtcacc gcttggtatc gaagcacaag cggcataagt 660
ccaaacactc caaagacatg gggttgggta ccccggaagc agcatccctg ggcacagtta 720
tcaaaccctt ggtggagtat gatgatatca gctctgattc cgacaccttc tccgatgaca 780
tggccttcaa actagaccga agggagaacg acgaacgtcg tggatcagat cggagcgacc 840
gcctgcacaa acatcgtcac caccagcaca ggcgttcccg ggacttacta aaagctaaac 900
agaccg                                     906

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<210> 63
 <211> 491
 <212> DNA
 <213> Homo sapiens

```

<400> 63
gacatgtttg cctgcagggg accagagaca atgggattag ccagtgtca ctgttcttta 60
tgcttcaga gaggatggg acagctctca ggtcagaatc caggctgaga aggccatgct 120
ggttgggggc ccccggaagc acggtccgga tcctccctgg catcagcgta gaccgctgc 180
tcaggcttgg ggtaccaaac tcagtctctg tactgttttg gccccatgct gtgagaggaa 240
aacctagaaa aagattgggt gtgctaagga atcagctgcc cctcatcct ccgcatcaa 300
tgctggtgac aacatattcc ctctcccagg acacagactc ggtgactcca cactgggctg 360
agtggcctct ggaggctcgt ggcctaaggc agggctccgt aaggctgatc ggctgaactg 420
ggtgggggtg gggtttctga ccttcgctt cccatcccat aaccgctgtc aatgagctca 480
cactgtggtc a                                     491

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<210> 64
 <211> 511
 <212> DNA
 <213> Homo sapiens

```

<400> 64
gatggcatgg tcgttgctaa tgtgcctgct gggatggagc acttccctct gtgagcccag 60
gggacccgcc tgtccctgga gcttggggca aggagggaag agtgatacca ggaagggtgg 120
gctgcagcca ggggccagag tcagttcagg gagtggctct cggccctcaa agctcctccg 180
gggactgctc aggagtgatg gtgcccctgga gtttgcccca acttccctgg ccaccctgga 240
aggtgcctgg ctgctccagg cctctaggct gggctgatgg gtttctccag gacacaagta 300
tcattaaagc caccctctcc tcagcttgtc aggcgcaca tgtgggacag gctgtgctca 360
caacccctc gcctgcctg cctccatca ggaggagcca gtggaacctt cggaaagctc 420
ccagcatctc agcagccctc aaaagtcgtc ctggggcaag ctctggttct cctgactgga 480
ggtcatctgg gcttggcctg ctctctctcg c                                     511

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<210> 65
 <211> 394
 <212> DNA
 <213> Homo sapiens

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<400> 65
taaaaaagtg taacaaaggt ttatttagac tttcttcatg ccccgagatc caggatgtct 60
atgtaaaccg ttatcttaca aagaaagcac aatatttggt ataaactaag tcagtactt 120
gcttaactga aatagcgtcc atccaaaagt gggtttaagg taaaactacc tgacgatatt 180
ggcggggatc ctgcagtttg gactgcttgc cgggtttgtc cagggttccg ggtctgttct 240
tggcactcat ggggacaggc atcctgctcg tctgtggggc cccgctggag cccttacgtg 300
aagctgaagg tatcgaccst agggggctct agggcagtgg gaccttcac cggaaactaac 360
aagggtcggg gagaggcctc ttgggctatg tggg                                     394

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<210> 66

<211> 359
 <212> DNA
 <213> Homo sapiens

<400> 66
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 tcacgttwaa gacactaggt cgggcgccac agtgccaccc aaggagaaga agaatttgga 120
 atttttccat gaagatgtac ggaaatctga tgttgaatat gaaaatggcc cccaaatgga 180
 attccaaaag gttaccacag gggctgtaag acctagtac cctcctaagt gggaaagagg 240
 aatggagaat agtatttctg atgcatcaag aacatcagaa tataaaactg agatcataat 300
 gaaggaaaat tccatatcca atatgagttt actcagagac agtagaaact attcccagg 359

<210> 67
 <211> 450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 425
 <223> n = A,T,C or G

<400> 67
 taggaataac aaatgtttat tcagaaatgg ataagtaata cataatcacc cttcatctct 60
 taatgcccct tcctctcctt ctgcacagga gacacagatg ggtaacatag aggcattgga 120
 agtggaggag gacacaggac tagccaccca cttctcttcc ccggtctccc aagatgactg 180
 cttatagagt ggaggaggca aacagggtccc ctcaatgtac cagatggtca cctatagcac 240
 cagctccaga tggccacgtg gttgcagctg gactcaatga aactctgtga caaccagaag 300
 atacctgctt tgggatgaga gggaggataa agccatgcag ggaggatatt taccatccct 360
 accctaagca cagtgcagc agtgagcccc cggtccccag tacctgaaaa accaaggcct 420
 actgnctttt ggatgctctc ttgggccacg 450

<210> 68
 <211> 511
 <212> DNA
 <213> Homo sapiens

<400> 68
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 gctgagaggc aagaccgtct ccctcctgct gcagctgctt cccacagcag cactgctggg 120
 cacagcagaa acgccagcag agaaaatggg agccgagagt ccttagccct ggagctgagg 180
 ctgcctcttg gctgaccgcg tggtgtacg tggccagAAC tggggttggc atctggcatc 240
 catTTgaggc cagggtggag gaaagggagg ccaacagagg aaaacctatt cctgctgtga 300
 caacacagcc cttgtccac gcagcctaag tgcagggagc gtgatgaagt caggcagcca 360
 gtcggggagg acgaggtaac tcagcagcaa tgtcaccttg tagcctatgc gctcaatggc 420
 ccggaggggc agcaacccc cgcacacgtc agccaacagc agtgccctcg caggcaccAA 480
 gagagcgatg atggacttga gcgccgtgtt c 511

<210> 69
 <211> 511
 <212> DNA
 <213> Homo sapiens

<400> 69
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 tatctgtcca ccattctgcc ttgcccttcc tggggctgag gcagacaaag gaaaggtaat 120
 gaggttaggg cccccaggcg ggctaagtgc tattggcctg ctctgtctca aagagagcca 180
 tagccagctg ggcacggccc cctagcccct ccagggtgct gaggcggcag cgggtggtaga 240

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gtttcttctact gagccgtggg ctgcagtcctc gcagggagaa cttctgcacc agccctggct 300
ctacggcccg aaagagggtgg agccctgaga accggaggaa aacatccatc acctccagcc 360
cctccagggc ttctctctct tcttgccctg ccagttcacc tgccagccgg gctcggggccg 420
ccaggtagtc agcgtttag aagcagccct ccgcagaagc ctgccggtca aatctccccg 480
ctataggagc cccccgggag gggtcagcac c 511

```

<210> 70

<211> 511

<212> DNA

<213> Homo sapiens

<400> 70

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caagttgaac gtcaggcttg gcagagggtgg agtgtagatg aaaacaaagg tgtgattatg 60
aagaggatgt gagtcctttg ggtgtaggag agaaaggctg ttgagcttct atttcaagat 120
acttttacct gtgcaaaaag cacattttcc acctccttct catggcattt gtgtaagggtg 180
agtatgattc ctattccatc tgcatttttag aggtgaagaa taacgtacaa gggattcagt 240
gattagcaag ggacccctca ctaagtgttg atggagtttag gacagagctc agctgtttga 300
atctcagagc ccaggcagct ggagctgggt aggatcctgg agctggcact aatgtgaggt 360
gcattccctc caaccaggc tcagatccgg aacctgaccg tgctgacccc cgaaggggag 420
gcagggctga gctggcccgt tgggtccct gtcctttca caccacactc tcgcttttag 480
gtgctgggct gggactactt cacagagcag c 511

```

<210> 71

<211> 511

<212> DNA

<213> Homo sapiens

<400> 71

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gcccctggag gagatctggc ctctctgtga tttcatcact gtgcacactc ctctcctgcc 180
ctccacgaca ggcttgctga atgacaacac ctttgccag tgcaagaagg ggtgctgtgt 240
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tggccagtgt gccggggctg cactggacgt gtttacggaa gagccgccac gggaccgggc 360
cttgggtggac catgagaatg tcatcagctg tccccacctg ggtgccagca ccaaggaggc 420
tcagagccgc tgtggggagg aaattgctgt tcagttcgtg gacatggtga aggggaaatc 480
tctcacgggg gttgtgaatg cccaggccct t 511

```

<210> 72

<211> 2017

<212> DNA

<213> Homo sapiens

<400> 72

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cgatgaatgg agggccaaat atgtgggcta ttacatctga agaacgtact aagcatgata 120
aacagtttga taacctcaaa ccttcaggag gttacataac aggtgatcaa gcccgactt 180
ttttctaca gtcaggctctg ccggccccgg ttttagctga aatatgggcc ttatcagatc 240
tgaacaagga tgggaagatg gaccagcaag agttctctat agctatgaaa ctcatcaagt 300
taaagttgca gggccaacag ctgcctgtag tcctccctcc tatcatgaaa caaccacct 360
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atcagccatt gcctccagtt gcacctatag caacacctt gtcttctgct acttcaggga 480
caagtattcc tcccctaagt atgcctgctc cctagtgc ttctgttagt acatcctcat 540
taccaaatgg taccgccagt ctcatcagc ctttatccat tccttattct tcttcaacat 600
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cagggaactc acctaagaca gggacctcag agtgggcagt tcctcagcct tcaagattaa 780
agtatcggca aaaatttaat agtctagaca aaggcatgag cggtacctc tcaggttttc 840

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```

aagctagaaa tgccttctt cagtcaaatt tctctcaaac tcagctagct actatttggg 900
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acctcactga catggccaaa gctggacagc cactaccact gacgttgccct cccgagcttg 1020
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catctaagct ctcagaaatg gattcattta acaatcagct gaaggaactc agagaaagct 1920
ataatacaca gcagttagcc cttgaacaac ttcataaaat caaacgtgac aaattgaagg 1980
aaatcgaaag aaaaagatta gagcaaaaaa aaaaaaa 2017

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<210> 73

<211> 414

<212> DNA

<213> Homo sapiens

<400> 73

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atggcagtg cattcaccat catgggaacc accttccctt ttcttcagga ttctctgtag 60
tggaagagag caccagtggt tgggctgaaa acatctgaaa gtaggagaa gaacctaaaa 120
taatcagtat ctccagagggc tctaagggtgc caagaagtct cactggacat ttaagtgcc 180
acaaaggcat actttcggaa tcgccaagtc aaaactttct aacttctgtc tctctcagag 240
acaagtgaga ctcaagagtc tactgcttta gtggcaacta cagaaaactg gtgttaccca 300
gaaaaaacagg agcaattaga aatgggtcca atatttcaaa gctccgcaaa caggatgtgc 360
tttcccttgc ccatttaggg tttcttctct ttcctttctc tttattaacc acta 414

```

<210> 74

<211> 1567

<212> DNA

<213> Homo sapiens

<400> 74

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atatctagaa gtctggagtg agcaacaag agcaagaaac aaaaagaagc caaaagcaga 60
aggctccaat atgaacaaga taaatctatc ttcaaagaca tattagaagt tgggaaaaata 120
attcatgtga actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 180
gcatccccag atctcaggga cctccccctg cctgtcacct ggggagtgag aggacaggat 240
agtgcattgt ctttgtctct gaatttttag ttatatgtgc tgtaatgttg ctctgaggaa 300
gcccctggaa agtctatccc aacatatcca catcttatat tccacaaatt aagctgtagt 360
atgtacccta agacgtgctc aattgactgc cacttcgcaa ctcaggggag gctgcatttt 420
agtaatgggt caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 480
ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa acagagcagt 540
cgggcagacc gattttataa ataaactgag caccttcttt ttaaacaac aaatgcgggt 600
ttattttctc gatgatgttc atccgtgaat ggtccaggga aggaccttc accttgacta 660
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acaggacgtc tccccattac aactacccaa tccgaagtgt caactgtgtc aggactaaga 960
aaccctggtt ttgagtagaa aagggcctgg aaagagggga gccacaacaa ctgtctgctt 1020

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cctcacatta gtcattggca aataagcatt ctgtctcttt ggctgctgcc tcagcacaga 1080
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cattctaccc tgcaagccaa gttctgtaag agaaatgcct gagttctagc tcagggttttc 1260
ttactctgaa tttagatctc cagacccttc ctggccacaa ttcaaattaa ggcaacaaac 1320
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gaggccttga ggaatgaagc tttgaaggaa aagaatactt tgtttccagc ccccttccca 1440
cactcttcat gtgttaacca ctgccttcct ggaccttgga gccacggtga ctgtattaca 1500
tgttgttata gaaaactgat tttagagttc tgatcgttca agagaatgat taaatataca 1560
tttccta
1567

```

<210> 75

<211> 240

<212> DNA

<213> Homo sapiens

<400> 75

```

tcgagcggcc gcccgggcag gtccttcaga cttggactgt gtcacactgc caggcttcca 60
gggctccaac ttgcagacgg cctgttggtg gacagtctct gtaatcgcg aagcaaccat 120
ggaagacctg ggggaaaaca ccatggtttt atccaccctg agatctttga acaacttcat 180
ctctcagcgt gcggaggagg gctctggact ggatatttct acctcggccg cgaccacgct 240

```

<210> 76

<211> 330

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 288

<223> n = A,T,C or G

<400> 76

```

tagcgyggtc gcggccgagg yctgcttytc tgtccagccc agggcctgtg gggtcagggc 60
ggtgggtgca gatggcatcc actccggtgg cttcccatc tttctctggc ctgagcaagg 120
tcagcctgca gccagagtac agagggccaa cactggtgtt cttgaacaag ggccttagca 180
ggccctgaag gcccctctct gtagtggtga acttcctgga gccaggccac atgttctcct 240
cataccgcag gytagygatg gtgaagttga ggggtgaaata gtattmangr agatggctgg 300
caracctgcc cgggcgggcc ctcsaaatcc
330

```

<210> 77

<211> 361

<212> DNA

<213> Homo sapiens

<400> 77

```

agcgtggtcg cgcccgaggt gtccttcagg gtctgcttat gcccttggtc aagaacacca 60
gtgtcagctc tctgtactct ggttgcagac tgaccttgct caggcctgag aaggatgggg 120
cagccaccag agtggatgct gtctgcaccc atcgtcctga ccccaaaagc cctggactgg 180
acagagagcg gctgtactgg aagctgagcc agctgaccca cggcactact gagctggggc 240
cctacaccct ggacagggac agtctctatg tcaatggttt caccatcgg agctctgtac 300
ccaccaccag caccgggggtg gtcagcgagg agccattcaa cctgcccggg cggccgctcg 360
a
361

```

<210> 78

<211> 356

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 7, 346, 350, 353

<223> n = A,T,C or G

<400> 78

```

ttggggnttt mgagcggccg cccgggcagg taccgggggtg gtcagcgagg agccattcac 60
actgaacttc accatcaaca acctgcggta tgaggagAAC atgcagcacc ctggctccag 120
gaagttcaac accacggaga gggctccttca gggcctgctc aggtccctgt tcaagagcac 180
cagtgttggc cctctgtact ctggctgcag actgactttg ctgagacttg agaaacatgg 240
ggcagccact ggagtggacg ccatctgcac cctccgcctt gatccactg gtcctggact 300
ggacagagag cggctatact gggagctgag ccagtcctct ggcgngacn ccnctt 356

```

<210> 79

<211> 226

<212> DNA

<213> Homo sapiens

<400> 79

```

agcgtggctg cggccgaggt ccagtcgcag catgctcttt ctctgcca ctggcacagt 60
gaggaagatc tctgctgtca gtgagaaggc tgcattccac tgagatggca gtcaaaagtg 120
catttaatac acctaacgta tcgaacatca tagcttggcc caggttatct catatgtgct 180
cagaacactt acaatagcct gcagacctgc ccgggcggcc gctcga 226

```

<210> 80

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 23

<223> n = A,T,C or G

<400> 80

```

tgtggtgttg aacttcctgg agncaggggtg acccatgtcc tccccatact gcaggttggt 60
gatggtgaag ttgaggggtga atggtaccag gagagggcca gcagccataa ttgtsgrgck 120
gsmgmssgag gmwggwgtty cwagggttcy rarrtccact gtggagggtcc caggagtgtc 180
ggtggtgggc acagagstcy gatgggtgaa accattgaca tagagactgt tcctgtccag 240
ggtgtagggg cccagctctt yratgycatt ggycagttkg ctyagctccc agtacagccr 300
ctctckgyyg mgwccagsgc ttttggggtc aagatgatgg atgcagatgg catccactcc 360
agtggctgct ccatccttct cggacctgag agaggtcagt ctgcagccag agtacagagg 420
gccaacactg gtgttctttg aata 444

```

<210> 81

<211> 310

<212> DNA

<213> Homo sapiens

<400> 81

```

tcgagcggcc gcccgggcag gtcaggaagc acattggtct tagagccact gcctcctgga 60
ttccacctgt gctgcggaca tctccaggga gtgcagaagg gaagcaggtc aaactgctca 120
gatcagtcag actggctgtt ctgattctc acctgagcaa ggtcagtctg cagccagagt 180
acagagggcc aacactggtg ttcttgaaca agggcttgag cagaccctgc agaaccctct 240
tccgtgggtg tgaacttcct ggaaaccagg gtgttgcatg ttttctctca taatgcaagg 300
ttggtgatgg 310

```

<210> 82
 <211> 571
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 202
 <223> n = A,T,C or G

<400> 82
 acgggtttcaa tggacacttt tattgttttac ttaatggatc atcaattttg tctcactacc 60
 tacaaatgga atttcatctt gtttccatgc tgagtagtga aacagtgaca aagctaataca 120
 taataaccta catcaaaaga gaactaagct aacactgctc actttctttt taacaggcaa 180
 aatataaata tatgactctt anaatgcaca atgggtttagt cactaaaaaa ttcaaattggg 240
 atcttgaaga atgtatgcaa atccagggtg cagtgaagat gagctgagat gctgtgcaac 300
 tgtttaaggg ttccctggcac tgcattctctt ggcoactagc tgaatcttga catggaaggt 360
 ttttagctaata gccaagtggg gatgcagaaa atgctaagtt gacttagggg ctgtgcacag 420
 gaactaaaag gcaggaaagt actaaatatt gctgagagca tccaccccag gaaggacttt 480
 accttccagg agctccaaac tggcaccacc cccagtgtct acatggctga ctttatctctc 540
 cgtgttccat ttggcacagc aagtggcagt g 571

<210> 83
 <211> 551
 <212> DNA
 <213> Homo sapiens

<400> 83
 aaggctggtg ggtttttgat cctgctggag aacctccgct ttcattgtgga ggaagaaggg 60
 aagggaagaag atgcttcttg gaacaagggt aaagccgagc cagccaaaat agaagctttc 120
 cgagcttcac ttccaagct aggggatgtc tatgtcaatg atgcttttgg cactgctcac 180
 agagcccaca gctccatggt aggagtcaat ctgccacaga aggctggtgg gtttttgatg 240
 aagaaggagc tgaactactt tgcaaaggcc ttggagagcc cagagcgacc cttcctggcc 300
 atcctgggag gagctaaagt tgcagacaag atccagctca tcaataatat gctggacaaa 360
 gtcaatgaga tgattatttg tgggtggaatg gcttttacct tccttaaggt gctcaacaac 420
 atggagattg gcacttctct gtttgatgaa gagggagcca agattgtcaa agacctaata 480
 tccaaagctg agaagaatgg tgtgaagatt accttgctg ttgactttgt cactgctgac 540
 aagtttgatg a 551

<210> 84
 <211> 571
 <212> DNA
 <213> Homo sapiens

<400> 84
 ttgttctctt acatttttct aaagagttac ttaaatacagt caactggtct ttgagactct 60
 taagtctctga ttccaactta gctaattcat tctgagaact gtggtatagg tggcgtgtct 120
 cttctagctg ggacaaaagt tctttgtttt cccctgtag agtatcacag accttctgct 180
 gaagctggac ctctgtcttg gccttggaact cccaaatctg cttgtcatgt tcaagcctgg 240
 aaatgttaat ctttaattct tccatatgga tggacatctg tctaagttga tccttttagaa 300
 cactgcaatt atcttctttg agtctaattt cttcttcttt gctttgaatc gcatcactaa 360
 acttctcttc ccatttctta gcttcatcta tcacctgtc acgatcatcc tggagggaag 420
 acatgctctt agtaaaggct gcaagctggg tcacagtact gtccaagttt tcctgaagtt 480
 gctgaacttc cttgtctttc ttgttcaaag taacctgaat ctctccaatt gtctcttcca 540
 agtggacttt ttctctgcgc aaagcatcca g 571

<210> 85

<211> 561
 <212> DNA
 <213> Homo sapiens

<400> 85
 tcattgcctg tgatggcatc tggaaatgtga tgagcagcca ggaagttgta gatttcattc 60
 aatcaaagga ttcagcatgt ggtggaagct gtgaggcaag agaaacaaga actgtatggc 120
 aagttaagaa gcacagaggg aaacaagaag gagacagaaa agcagttgca ggaagctgag 180
 caagaaatgg aggaaatgaa agaaaagatg agaaagtgtg ctaaatctaa acagcagaaa 240
 atoctagagc tggagaaga gaatgaccgg cttagggcag aggtgcaccc tgcaggagat 300
 acagctaaag agtgtatgga aacacttctt tcttccaatg ccagcatgaa ggaagaactt 360
 gaaaggggtca aaatggagta tgaaaccctt tctaagaagt ttcagtcttt aatgtctgag 420
 aaagactctc taagtgaaga gggtcaagat ttaaagcatc agatagaagg taatgtatct 480
 aaacaagcta acctagaggg caccgagaaa catgataacc aaacgaatgt cactgaagag 540
 ggaacacagt ctataccagg t 561

<210> 86
 <211> 795
 <212> DNA
 <213> Homo sapiens

<400> 86
 aagccaataa tcaccattta ttacttaata tatgccaaacc actgtacttg gcagttcaca 60
 aattctcacc gttacaacaa ccccatgagg tattttattcc cattctatag atagggaac 120
 cacagctcaa gtaagttagg aaactgagcc aagtatacac agaatacgaa gtggcaaac 180
 tagaaggaag gactgacact gctatctgct ggccctcagt gtcctggctc ttttcacacg 240
 gggtcaatgt ctccagcgct gctgctgctg ctgcattacc atgccctcat tgtttttctt 300
 cctctgggtg tcaactgcat ccttcaaaga atctaactca ttccagagac cacttatttc 360
 tttctctctt tctgaaatta cttttaataa ttcttcatga gggggaaaag aagatgcctg 420
 ttggtagttt tgttgtttta gctgctcaat ttgggactta aacaatttgt tttcatcttg 480
 tacatcctgt aacagctgtg ttttgctaga aagatcactc tccctctctt ttagcatggc 540
 ttctaacctc ttcaattcat tttccttttc ttcaacaca atctcaagtt cttcaaactg 600
 tgatgcagaa gaggcctctt tcaagttatg ttgtgctact tcctgaacat gtgcttttaa 660
 agattcattt tcttcttgaa gatcctgtaa ccacttcctt gtattggcta ggtctttctc 720
 tttctcttcc aaaacagcct tcatggtatt catctgttcc tcttttcctt ttaataagtt 780
 caggagcttc agaac 795

<210> 87
 <211> 594
 <212> DNA
 <213> Homo sapiens

<400> 87
 caagcttttt tttttttttt aaaaagtgtt agcattaatg ttttattgtc acgcagatgg 60
 caactgggtt tatgtcttca ttttttatat ttttgtaaatt taaaaaaatt acaagtttta 120
 aatagccaat ggctgggttat attttcagaa aacatgatta gactaattca ttaatgggtg 180
 cttcaagctt ttctttattg gctccagaaa attcaccac cttttgtccc ttcttaaaaa 240
 actggaatgt tggcatgcat ttgacttcac actctgaagc aacatcctga cagtcattca 300
 catctacttc aaggaatatc acgttggaat acttttcaga gaggggaatga aagaaaggct 360
 tgatcatttt gcaaggccca caccacgtgg ctgagaagtc aactactaca agtttatcac 420
 ctgcagcgct caaggcttcc tgaaaagcag tcttgctctc gatctgcttc accatcttgg 480
 ctgctggagt ctgacgagcg gctgtaagga ccgatggaaa tggatccaaa gcaccaaaca 540
 gagcttcaag actcgtgctt tggcttgaat tcggatccga tatcgccatg gcct 594

<210> 88
 <211> 557
 <212> DNA
 <213> Homo sapiens

```

<400> 88
aagtgttagc attaatgttt tattgtcacg cagatggcaa ctgggtttat gtcttcatat 60
tttatatttt tgtaaatata aaaaattmca agtttttaaat agccaatggc tggttatat 120
ttcagaaaaac atgattagac taattcatta atgggtggctt caagcttttc cttattggct 180
ccagaaaaatt caccacacct ttgtcccttc ttaaaaaact ggaatgttg catgcatttg 240
acttcacact ctgaagcaac atcctgacag tcatccacat ctacttcaag gaatatcacg 300
ttggaataact tttcagagag ggaatgaaag aaaggcttga tcattttgca aggccacac 360
cacgtggctg agaagtcaac tactacaagt ttatcacctg cagcgtccaa ggcttcctga 420
aaagcagtct tgctctcgat ctgcttcacc atcttggctg ctggagtctg acgagcggct 480
gtaaggaccg atggaaatgg atccaaagca ccaaacagag cttcaagact cgctgcttgg 540
catgaattcg gatccga
557

```

```

<210> 89
<211> 561
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 544, 551
<223> n = A,T,C or G

```

```

<400> 89
tacaaacttt attgaaacgc acacgcgcac acacacaaac acccctgttg atagggaana 60
gcacctggcc acaggggtcca ctgaaacggg gaggggatgg cagcttgtaa tgtggctttt 120
gccacaaccc cttcttgaca gggaaggcct tagattgagg cccacacctc catgggtgatg 180
gggagctcag aatgggggtcc agggagaatt tgggttagggg gaggtgctag ggaggcatga 240
gcagagggca ccctcagagt ggggtcccga gggctgcaga gtcttcagta ctgtccctca 300
cagcagctgt ctcaaggctg ggtccctcaa aggggcgtcc cagcgcgggg cctccctgcg 360
caaacacttg gtaccccttg ctgcgcagcg gaagccagca ggacagcagt ggcgccgatc 420
agcacaacag acgccctggc ggtagggaca gcaggcccag ccctgtcggg tgtctcggca 480
gcaggtcttg ttatcatggc agaagtgtcc ttccacact tcacgtcctt cacaccacag 540
tganngctac nggccaggaa g
561

```

```

<210> 90
<211> 561
<212> DNA
<213> Homo sapiens

```

```

<400> 90
cccgtgggtg ccatccacgg agttgttacc tgatcttttg aagcaggatc gcccgctctgc 60
actgcagtgg aagccccgtg ggcagcagtg atggccatcc ccgcatgcca cggcctctgg 120
gaagggggcag caactggaag tccctgagac ggtaaagatg caggagtggc cggcagagca 180
gtgggcatca acctggcagg ggcaaccacg atgcctgctc agtggttggt gccatttgct 240
cagaagggga cggcagcagc tgtagctggc tcctccgggg tccaggcagc aggccacagg 300
gcagaactga ccatctgggc accgcgttcc agccaccagc cctgctgtta aggccacca 360
gtccaccagg gtccacatgg tctgcctgcg tccgaactcc cggtccttgg gccctgatgg 420
ttctacctgc tgtgagctgc ccagtgggaa gtatggctgc tgccaatgcc caacgccacc 480
tgctgctccg atcacctgca ctgctgcccc aagacactgt gtgtgacctg atccagagta 540
agtgcctctc caaggagaac g
561

```

```

<210> 91
<211> 541
<212> DNA
<213> Homo sapiens

```

```

<220>

```

<221> misc_feature
 <222> 480, 491
 <223> n = A,T,C or G

<400> 91
 gaatcacctt tctgggtttag ctagtacttt gtacagaaca atgaggtttc ccacagcgga 60
 gtctccctgg gctctgtttg gctctcggtg aggcaggcct acaccttttc ctctcctcta 120
 tggagagggg aatatgcatt aagggtgaaaa gtcaccttcc aaaagtgaga aagggtattcg 180
 attgctgctt caggactgtg gaattatttg gaatgtttta caaatgggtg ctacaaaaca 240
 acaaaaaagg taattacaaa atgtgtacat cacaacatgc tttttaaaga cattatgcat 300
 tgtgctcaca ttcccttaaa tgttggtttcc aaagggtgctc agcctctagc ccagctggat 360
 tctccgggaa gaggcagaga cagtttggtg aaaaagacac agggaaggag ggggtggtga 420
 aaggagaaag cagccttcca gttaaagatc agccctcagt taaaggtcag cttcccgcan 480
 gctggcctca ngcggagtct gggtcagagg gaggagcagc agcaggggtg gactggggcg 540
 t 541

<210> 92
 <211> 551
 <212> DNA
 <213> Homo sapiens

<400> 92
 aaccggagcg cgagcagtag ctgggtgggc accatggctg ggatcaccac catcgaggcg 60
 gtgaagcgca agatccaggt tctgcagcag caggcagatg atgcagagga gcgagctgag 120
 cgctccagc gagaagttga gggagaaagg cgggcccggg aacaggctga ggctgaggtg 180
 gctccttga accgtaggat ccagctggtt gaagaagagc tggaccgtgc tcaggagcgc 240
 ctggccactg ccctgcaaaa gctggaagaa gctgaaaaag ctgctgatga gagtggagaga 300
 ggtatgaagg ttattgaaaa ccgggcctta aaagatgaag aaaagatgga actccaggaa 360
 atccaactca aagaagctaa gcacattgca gaagaggcag ataggaagta tgaagaggtg 420
 gctcgtaagt tgggtgatcat tgaaggagac ttggaacgca cagaggaacg agctgagctg 480
 gcagagtccc gttgccgaga gatggatgag cagattagac tgatggacca gaacctgaag 540
 tgtctgagtg c 551

<210> 93
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 93
 gagaaacttg cctttattgt gggcccagga gggcacaaa gtcaggaggc ccaagggagg 60
 gatctgggtt tctggatagc cagggtcatag catgggtatc agtaggaatc cgctgtagct 120
 gcacaggcct cacttgctgc agttccgggg agaacacctg cactgcatgg cgttgatgac 180
 ctggtggtac acgacagagc cattggtgca gtgcaagggc acgcgcatgg gctccgtcct 240
 cgagggcagg cagcaggagc attgctcctg cacatcctcg atgtcaatgg agtacacagc 300
 tttgctggca cactttccct ggcagtaatg aatgtccact tcctcttggg acttacaatc 360
 tcccactttg atgtactgca ccttggtgtg gatgtctttg caatcaggct cctcacatgt 420
 gtcacagcag gtgcctggaa ttttcacgat tttgcctcct tcagccagac acttggtgtc 480
 atcaaatggg gggcagcccg tgacctctct ctcccagatg tactctctct t 531

<210> 94
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 517
 <223> n = A,T,C or G

```

<400> 94
gcctggacct tgccggatca gtgccacaca gtgacttgct tggcaaattg ccagaccttg 60
ctgcagagtc atcgtgtcaa ttgtgacctt ggaccccggc cttcatgtgc caacagccag 120
tctcctgttc ggggtggagga gacgtgtggc tgccgctgga cctgcccttg tgtgtgcacg 180
ggcagttcca ctccggcacat cgtcaccttc gatgggcaga atttcaagct tactggtagc 240
tgctcctatg tcatctttca aaacaaggag caggacctgg aagtgtcctt ccacaatggg 300
gcctgcagcc ccggggcaaaa acaagcctgc atgaagtcca ttgagattaa gcatgctggc 360
gtctctgctg agctgcacag taacatggag atggcagtgg atgggagact ggtccttgcc 420
ccgtacgttg gtgaaaacat ggaagtcagc atctacggcg ctatcatgta tgaagtcagg 480
tttaccatc ttggccacat cctcacatac accgcncnaa aacaacgagt t 531

```

```

<210> 95
<211> 605
<212> DNA
<213> Homo sapiens

```

```

<400> 95
agatcaacct ctgctggtea ggaggaatgc cttccttgct ttggatcttt gctttgacgt 60
tctcgatagt rwcaactkk r ytsramskma agkgyratgr wmttksyw gw rasyktmwwm 120
rsgraraytt agacaycccm cctcwagagac gsagkaccar gtgcagaggt ggactctttc 180
tggtatgttg agtcagacag ggtgcgtcca tcttccagct gtttcccagc aaagatcaac 240
ctctgctgat caggagggat gccttcctta tcttggatct ttgccttgac attctcgatg 300
gtgtcactgg gctccacctc gaggggtgat gtcttaccag tcagggctct cacaagaty 360
tgcacccac ctctgagacg gagcaccagg tgcagggtrg actctttctg gatgtttag 420
tcagacaggg tgcgyccatc ttccagctgc tttccsagca aagatcaacc tctgctggc 480
aggaggratg ccttccttgt cytggatctt tgcyttgacr ttctcratgg tgtcactcgg 540
ctccacttcg agagtgatgg tcttaccagt cagggtcttc acgaagatct gcatccacc 600
tctaa 605

```

```

<210> 96
<211> 531
<212> DNA
<213> Homo sapiens

```

```

<400> 96
aagtcacaaa cagacaaaga ttattaccag ctgcaagcta tattagaagc tgaacgaaga 60
gacagaggtc atgattctga gatgattgga gacottcaag ctogaattac atctttacaa 120
gaggaggtga agcatctcaa acataatctc gaaaaagtgg aaggagaaag aaaagaggct 180
caagacatgc ttaatcactc agaaaaggaa aagaataatt tagagataga tttaactac 240
aaacttaaat cattacaaca acggttagaa caagaggtaa atgaacacaa agtaaccaa 300
gctcgtttta ctgacaaaca tcaatctatt gaagaggcaa agtctgtggc aatgtgtgag 360
atggaaaaaa agctgaaaga agaaagagaa gctcgagaga aggctgaaaa tcgggttggt 420
cagattgaga aacagtgttc catgctagac gttgatctga agcaatctca gcagaaacta 480
gaacatttga ctggaaataa agaaaggatg gaggatgaag ttaagaatct a 531

```

```

<210> 97
<211> 1017
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 963, 995, 1001, 1008, 1010
<223> n = A,T,C or G

```

```

<400> 97
cgctccacc atgtccatca gggtgacca gaagtcctac aagggtgtcca cctctggccc 60

```

```

ccgggccttc agcagccgct cctacacgag tgggcccgggt tcccgcacatca gctcctcgag 120
cttctccccga gtgggcagca gcaactttcg cggtggcctg ggcgccggct atggtggggc 180
cagcggcatg ggaggcatca ccgcagttac ggtcaaccag agcctgctga gcccccttgt 240
cctggaggtg gaccccaaca tccaggccgt gcgcaccag gagaaggagc agatcaagac 300
cctcaacaac aagtttgctt ccttcacaga caaggtacgg ttcctggagc agcagaacaa 360
gatgctggag accaagtgga gcctcctgca gcagcagaag acggctcgaa gcaacatgga 420
caacatgttc gagagctaca tcaacarcct taggcggcag ctggagactc tgggccagga 480
gaagctgaag ctggaggcgg agcttggaac catgcagggg ctggtggagg acttcaagaa 540
caagtatgag gatgagatca ataagcgtac agagatggag aacgaatttg tcctcatcaa 600
gaaggatgtg gatgaagctt acatgaacaa ggtagagctg gagtctcgcc tgggaagggt 660
gaccgacgag atcaacttcc tcaggcagct gtatgaagag gagatccggg agctgcagtc 720
ccagatctcg gacacatctg tgggtgctgc catggacaac agccgctccc tggacatgga 780
cagcatcatt gctgaggtca aggcacagta cgaggatatt gccaacgcga gccgggctga 840
ggctgagagc atgtaccagg tcaagtatga ggagctgcag agcctggctg ggaagcacgg 900
ggatgacctg cggcgacaaa agactgagat ctctgagatg aacccggaac atcagcccgg 960
ctncaggctg agattgaggg cctcaaaggc caganggctt ncctggangn ccgccat 1017

```

<210> 98

<211> 561

<212> DNA

<213> Homo sapiens

<400> 98

```

cccggagcca gccaacgagc ggaaaatggc agacaatttt tcgctccatg atgcgttattc 60
tgggtctgga aacccaaacc ctcaaggatg gcctggcgca tgggggaacc agcctgctgg 120
ggcagggggc taccagggg cttcctatcc tggggcctac cccgggcagg ccccccagg 180
ggcttatcct ggacaggcac ctccaggcgc ctaccctgga gcacctggag ctatatccgg 240
agcacctgca cctggagtct acccagggcc acccagcggc cctggggcct acccatcttc 300
tggacagcca agtgccaccg gagcctaccc tgccactggc ccctatggcg cccctgctgg 360
gccactgatt gtgccttata acctgccttt gcctggggga gtggtgcctc gcatgctgat 420
aacaattctg ggacagggtga agcccaatgc aaacagaatt gcttttagatt tccaaagagg 480
gaatgatgtt gccttccact ttaaccacag cttcaatgag aacaacagga gagtcatagg 540
ttgcaataca aagctggata a

```

<210> 99

<211> 636

<212> DNA

<213> Homo sapiens

<400> 99

```

gggaatgcaa caactttatt gaaaggaaag tgcaatgaaa tttgttgaaa ccttaaaagg 60
ggaaacttag acaccccccc tcragcgmag kaccargtgc aragggtggac tctttctgga 120
tggtgtagtc agacagggtg cgwccatctt ccagctgttt yccrgcaaag atcaacctct 180
gctgatcagg aggratgcct tccttatctt ggatctttgc cttgacattc tcgatgggtg 240
cactgggctc cacctcgagg gtgatgggtc taccagtcag ggtcttcacg aagatytgca 300
tcccacctct gagacggagc accagggtgca gggtrgactc tttctggatg ttgtagtcag 360
acaggggtgcg yccatcttcc agctgctttc csagcaaaga tcaacctctg ctggtcagga 420
ggratgcctt ccttgctcytg gatctttgcy ttgacrttct caatgggtgct actcggtccc 480
acttcgagag tgatgggtctt accagtcagg gtcttcacga agatctgcat cccacctcta 540
agacggagca ccagggtgcag ggtggactct ttctggatgg ttgtagtcag acaggggtgcg 600
tccatcttcc agctgtttcc cagcaaagat caacct

```

<210> 100

<211> 697

<212> DNA

<213> Homo sapiens

<400> 100

```

aggttgatct ttgctgggaa acagctggaa gatggacgca ccctgtctga ctacaaccat 60
ccagaaagag tccaccctgc acctggtgct ccgtcttaga ggtgggatgc agatcttcgt 120
gaagaccctg actggttaaga ccatcactct cgaagtggag ccgagtgaca ccattgagaa 180
ygtcaargca aagatccarg acaaggaagg catycctcct gaccagcaga ggttgatctt 240
tgctsggaaa gcagctggaa gatgggacga ccctgtctga ctacaacatc cagaaagagt 300
cyaccctgca cctggtgctc cgtctcagag gtgggatgca ratcttcgtg aagaccctga 360
ctggttaagac catcaccctc gaggtggagc ccagtgaacac catcgagaat gtcaaggcaa 420
agatccaaga taaggaaggc atccctcctg atcagcagag gttgatcttt gctgggaaac 480
agctggaaga tggacgcacc ctgtctgact acaacatcca gaaagagtcc acctytgcac 540
ytggtmctbc gtctyagagg kgggrtgcaa atctwmgtkw agacactcac tkkyaagryy 600
atcamcmwtg akktcgakys castkwact wtcrakaamg tyrwwgcawa gatccmagac 660
aaggaaggca ttcctcctga ccagcagagg ttgatct 697

```

<210> 101

<211> 451

<212> DNA

<213> Homo sapiens

<400> 101

```

atggagtctc actctgtcga ccaggctgga gcgctgtggt gcgatatcgg ctcaactgcag 60
tctccacttc ctgggttcaa gcgatcctcc tgcctcagcc tcccgagtag ctgggactac 120
aggcaggcgt caccataatt ttgtatctt tagtagagac atggtttcgc catgttggtc 180
gggctggtct cgaactcctg acctcaagtg atctgtcctg gcctcccaa gtgttggtg 240
tacaggcgaa agccaacgct cccggccagg gaacaacttt agaatgaagg aaatatgcaa 300
aagaacatca catcaaggat caattaatta ccactctatta attactatat gtgggtaatt 360
atgactatct cccaagcatt ctacgttgac tgcttgagaa gatgtttgtc ctgcatggtg 420
gagagtggag aaggggccagg attcttaggt t 451

```

<210> 102

<211> 571

<212> DNA

<213> Homo sapiens

<400> 102

```

agcgcggtct tccggcgcga gaaagctgaa ggtgatgtgg ccgccctcaa ccgacgcac 60
cagctcggtt agggagggtt ggacagggct caggaacgac tggccacggc cctgcagaag 120
ctggaggagg cagaaaaagc tgcatgatg agtgagagag gaatgaagg gatagaaaac 180
cgggccatga aggatgagga gaagatggag attcaggaga tgcagctcaa agaggccaag 240
cacattgcgg aagaggctga ccgcaaatac gaggaggtag ctctgaagct ggtcatcctg 300
gagggtgagc tggagagggc agaggagcgt gcggagggtg ctgaactaaa atgtggtgac 360
ctggaagaag aactcaagaa tgttactaac aatctgaaat ctctggaggc tgcatctgaa 420
aagtattctg aaaaggagga caaatatgaa gaagaaatta aacttctgtc tgacaaactg 480
aaagaggctg agaccctgac tgaatttgca gagagaacgg ttgcaaaact ggaaaagaca 540
attgatgacc tgggaagagaa acttgcccag c 571

```

<210> 103

<211> 451

<212> DNA

<213> Homo sapiens

<400> 103

```

gtgcacaggt cccatcttatt gtagaaaata ataataatta cagtgatgaa tagctcttct 60
taaattacaa aacagaaacc acaagaagg aagaggaaaa accccaggac ttccaagggt 120
gaagctgtcc cctctcctcc gccaccctcc caggctcatt agtgccttg gaaggggacag 180
aggactcaga ggggatacgt ctccaggggc cctgggctga agcgggtgag gcagagagtc 240
ctgaggccac agagctgggc aacctgagcc gcctctctgg cccctcccc caccactgcc 300
caaacctgtt tacagcacct tcgcccctcc cctctaaacc cgtccatcca ctctgcactt 360
cccaggcagg tgggtggggc aggcctcagc catactcctg ggcgcgggtt tcggtgagca 420

```

aggcacagtc ccagagggtga tatcaaggcc t

451

<210> 104

<211> 441

<212> DNA

<213> Homo sapiens

<400> 104

```
gcaaggaact ggtctgctca cacttgctgg cttgcgcatac aggactggct ttatctcctg 60
actcacgggtg caaagggtgca ctctgcgaac gtttaagtccg tccccagcgc ttggaatcct 120
acggcccccac cagccggatc ccctcagcct tccaggctcct caactcccgt ggacgctgaa 180
caatggccctc catggggcta caggtaatgg gcatcgcgct ggccgtcctg ggctggctgg 240
ccgtcatgct gtgctgcgcg ctgcccatgt ggcgcgtgac ggcccttcac ggagcaaca 300
ttgtcacctc gcagaccatc tgggagggcc tatggatgaa ctgcgtgggtg cagagcaccg 360
gccagatgca gtgcaagggtg tacgactcgc tgctggcact gccgcaggac ctgcaggcgg 420
cccgccgacct cgtcatcacc a
```

441

<210> 105

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 195

<223> n = A,T,C or G

<400> 105

```
tgcaaaaggg acacaggggt tcaaaaataa aaattttctct tccccctccc caaacctgta 60
ccccagctcc ccgaccacaa ccccttcctt ccccgggga aagcaagaag gagcagggtg 120
ggcatctgca gctgggaaga gagaggccgg ggagggtgcc agctcgggtg tgggtctctt 180
ccaaatataa atacntgtgt cagaactgga aaatcctcca gcacccacca cccaagcact 240
ctccgttttc tgccggtggt tggagagggg cggggggcag gggcgccagg caccggctgg 300
ctgcggtcta ctgcatccgc tgggtgtgca ccccgcgagc ctccctgctg tcattgtaga 360
agagatgaca ctccgggtcc ccccggtatg tgggggctcc ctggatcagc ttcccggtgt 420
tgggggttac acaccagcac tcccacgctt gcccggtcag agacatcttg cactgtttga 480
ggttgtacag gccatgcttg tcacagttg
```

509

<210> 106

<211> 571

<212> DNA

<213> Homo sapiens

<400> 106

```
gggttgagg gactggttct ttatttcaaa aagacacttg tcaatattca gtatcaaaac 60
agttgcacta ttgatttctc tttctcccaa tcggccccaa agagaccaca taaaaggaga 120
gtacatttta agccaataag ctgcaggatg tacacctaac agacctccta gaaaccttac 180
cagaaaatgg ggactgggta gggaaggaaa cttaaaagat caacaaactg ccagcccacg 240
gactgcagag gctgtcacag ccagatgggg tggccagggt gccacaaacc caaagcaaag 300
tttcaaaata atataaaatt taaaaagttt tgtacataag ctattcaaga tttctccagc 360
actgactgat acaaagcaca attgagatgg cacttctaga gacagcagct tcaaaccacg 420
aaaagggtga tgagatgagt ttcacatggc taaatcagtg gcaaaaacac agtcttcttt 480
ctttctttct ttcaaggagg caggaaagca attaagtggc cacctcaaca taagggggac 540
atgatccatt ctgtaagcag ttgtgaagg g
```

571

<210> 107

<211> 555

<212> DNA

<213> Homo sapiens

<400> 107

```

caggaaccgg agcgcgagca gtagctgggt gggcaccatg gctgggatca ccaccatcga 60
ggcgggtgaag cgcaagatcc aggttctgca gcagcaggca gatgatgcag aggagcgagc 120
tgagcgcttc cagcgagaag ttgagggaga aaggcgggcc cggaacagg ctgaggctga 180
ggtggcctcc ttgaaccgta ggatccagct ggttgaagaa gagctggacc gtgctcagga 240
gcgcctggcc actgccctgc aaaagctgga agaagctgaa aaagctgctg atgagagtga 300
gagaggtatg aaggttattg aaaaccgggc cttaaaagat gaagaaaaga tggaaactcca 360
ggaaatccaa ctcaaagaag ctaagcacat tgcagaagag gcagatagga agtatgaaga 420
ggtggctcgt aagttggtga tcattgaagg agacttgga cgcacagagg aacgagctga 480
gctggcagag tcccgttgcc gagagatgga tgagcagatt agactgatgg accagaacct 540
gaagtgtctg agtgc                                     555

```

<210> 108

<211> 541

<212> DNA

<213> Homo sapiens

<400> 108

```

atctacgtca tcaatcaggc tggagacacc atgttcaatc gagctaagct gctcaatatt 60
ggctttcaag aggccttgaa ggactatgat tacaactgct ttgtgttcag tgatgtggac 120
ctcattccga tggacgaccg taatgcctac aggtgttttt cgcagccacg gcacatttct 180
gttgcaatgg acaagttcgg gtttagcctg ccatatgttc agtatatttg aggtgtctct 240
gctctcagta aacaacagtt tcttgccatc aatggattcc ctaataatta ttggggtttg 300
ggaggagaag atgacgacat ttttaacaga ttagttcata aaggcatgtc tatatcacgt 360
ccaaatgctg tagtagggag gtgtcgaatg atccggcatt caagagacaa gaaaaatgag 420
cccaatcctc agaggtttga ccggatcgca catacaaagg aaacgatgcg cttcgatggg 480
ttgaactcac ttacctacaa ggtgttgga gtcagagata cccgttatat acccaaata 540
c                                     541

```

<210> 109

<211> 411

<212> DNA

<213> Homo sapiens

<400> 109

```

ctagacctct aattaaaagg cacaatcatg ctggagaatg aacagtctga ccccgagggc 60
cacagcgaat tttagggaag gaggcaaaga ggtgagaagg gaaaggaaag aaggaaggaa 120
ggagaacaat aagaactgga gacgttgggt gggtcaggga gtgtggtgga ggctcggaga 180
gatggtaaac aaacctgact gctatgagtt ttcaacccca tagtctaggg ccatgagggc 240
gtcagttctt ggtggctgag ggtccttcca ccagccccc ctgggggagt ggagtgggga 300
gttctgccag gtaagcagat gttgtctccc aagttcctga cccagatgtc tggcaggata 360
acgctgacct gttccctcaa caaggacact gaaagtaatt ttgctcttta c 411

```

<210> 110

<211> 451

<212> DNA

<213> Homo sapiens

<400> 110

```

ccgaattcaa gcgtcaacga tccytccctt accatcaaat caattggcca ccaatggtac 60
tgaacctacg agtacaccga ctacgggcgg actaatcttc aactcctaca tacttcccc 120
attattccta gaaccaggcg acctgcgact ccttgacgtt gacaatcgag tagtactccc 180
gattgtaagc cccattcgta taataattac atcacaagac gtcttgcact catgagctgt 240
ccccacatta ggcttaaaaa cagatgcaat tcccggacgt ctaagccaaa ccactttcac 300
cgctacacga ccgggggtat actacgggtc atgctctgaa atctgtggag caaaccacag 360
tttcatgccc atcgtcctag aattaattcc cctaaaaatc tttgaaatag ggcccgtatt 420

```

taccctatag caccctctct acccctcta g

451

<210> 111

<211> 541

<212> DNA

<213> Homo sapiens

<400> 111

```
gctcttcaca cttttattgt taattctctt cacatggcag atacagagct gtcgtcttga 60
agaccaccac tgaccaggaa atgccacttt tacaaaatca tcccccttt tcatgattgg 120
aacagttttc ctgaccgtct gggagcgttg aagggtgacc agcacatttg cacatgcaaa 180
aaaggagtga ccccaaggcc tcaaccacac ttcccagagc tcaccatggg ctgcagggtga 240
cttgccagggt ttgggggttc tgagctttcc ttgctgctgc ggtggggagg ccctcaagaa 300
ctgagaggcc ggggtatgct tcatgagtgt taacatttac gggacaaaag cgcattcatta 360
ggataaggaa cagccacagc acttcatgct tgtgagggtt agctgtagga gcgggtgaaa 420
ggattccagt ttatgaaaat ttaaagcaaa caacggtttt tagctgggtg ggaaacagga 480
aaactgtgat gtcggccaat gaccaccatt tttctgcca tgtgaaggtc cccatgaaac 540
c
```

<210> 112

<211> 521

<212> DNA

<213> Homo sapiens

<400> 112

```
caagcgcttg gcgtttggac ccagttcagt gaggttcttg ggttttgtgc ctttggggat 60
tttggtttga cccaggggtc agccttagga aggtcttcag gaggaggccg agttcccctt 120
cagtaaccac cctctctccc cactttccct ctcccggcaa catctctggg aatcaacagc 180
atattgacac gttggagccg agcctgaaca tgcccctcgg ccccgacaca tggaaaaccc 240
ccttcccttg ctaaggtgtc tgagtttctg gctcttgagg catttccaga cttgaaattc 300
tcatcagtcct attgctcttg agtctttgca gagaaacctc gatcagggtc acctggggaga 360
aagactttgt ccccaacttac agatctatct cctcccttgg gaagggcagg gaatggggac 420
ggtgtatgga ggggaaggga tctcctgcgc ccttcattgc cacacttggg gggaccatga 480
acatctttag tgtctgagct tctcaaatta ctgcaatagg a
```

<210> 113

<211> 568

<212> DNA

<213> Homo sapiens

<400> 113

```
agcgtcaaat cagaatggaa aagactcaaa accatcatca acaccaagat caaaaggaca 60
agratccttc aagaaacagg aaaaaactcc taaaacacca aaaggaccta gttctgtaga 120
agacattaaa gcaaaaatgc aagcaagtat agaaaaaggt ggttctcttc ccaaagtgga 180
agccaaattc atcaattatg tgaagaattg cttccggatg actgaccaag aggctattca 240
agatctcttg cagtggagga agtctcttta agaaaatagt ttaaacaatt tgttaaaaaa 300
ttttccgtct tatttcattt ctgtaacagt tgatatctgg ctgtcctttt tataatgcag 360
agtgagaact ttccctaccg tgtttgataa atgttgcca ggttctattg ccaagaatgt 420
gttgccaaa atgcctgttt agtttttaaa gatggaaact caccctttgc ttgggtttta 480
gtatgtatgg aatgttatga taggacatag tagtagcggg ggtcagacat ggaaatggtg 540
ggsmgacaaa aatatacatg tgaaataa
```

<210> 114

<211> 483

<212> DNA

<213> Homo sapiens

<400> 114

```

tccgaattcc aagcgaatta tggacaaacg attcctttta gaggattact tttttcaatt 60
tcgggttttag taatctaggc tttgcctgta aagaatacaa cgatggattt taaatactgt 120
ttgtggaatg tgtttaaagg attgattcta gaacctttgt atatttgata gtattttctaa 180
ctttcatttc tttactgttt gcagttaatg ttcatgttct gctatgcaat cgtttatatg 240
cacgttttct taattttttt agattttcct ggatgtatag tttaacaac aaaaagtcta 300
tttaaaactg tagcagtagt ttacagttct agcaaagagg aaagtgtgtg ggttaaactt 360
tgtattttct ttcttataga ggcttctaaa aagggtatttt tataatgttct ttttaacaaa 420
tattgtgtac aacctttaaa acatcaatgt ttggatcaaa acaagacca gcttattttc 480
tgc 483

```

<210> 115

<211> 521

<212> DNA

<213> Homo sapiens

<400> 115

```

tgtggtggcg cgggctgagg tggaggccca ggactctgac cctgcccctg ccttcagcaa 60
ggcccccgcc agcgccggcc actacgaact gccgtgggtt gaaaaatata ggccagtaaa 120
gctgaatgaa attgtcggga atgaagacac cgtgagcagg cttagaggtct ttgcaaggga 180
aggaaatgtg cccaacatca tcattgcggg ccctocagga accggcaaga ccacaagcat 240
tctgtgcttg gcccgggccc tgctgggccc agcactcaaa gatgccatgt tggaaactcaa 300
tgcttcaa at gacaggggca ttgacgttgt gaggaataaa attaaaatgt ttgctcaaca 360
aaaagtcact cttcccaaag gccgacataa gatcatcatt ctggatgaag cagacagcat 420
gaccgacgga gccagcaag ccttgaggag aaccatggaa atctactcta aaaccactcg 480
ttcgcccttg cttgtaatgc ttcggataag atcatcgagc c 521

```

<210> 116

<211> 501

<212> DNA

<213> Homo sapiens

<400> 116

```

ctttgcaaag cttttatttc atgtctgcgg catggaatcc acctgcacat ggcatcttag 60
ctgtgaagga gaaagcagtg cagcagaagg aatgagtggg cggaaccaac ggccctccaca 120
agctgccttc cagcagcctg ccaaggccat ggcagagaga gactgcaaac aaacacaagc 180
aaacagagtc tcttcacagc tggagtctga aagctcatag tggcatgtgt gaatctgaca 240
aaattaaaag tgtgcatagt ccattacatg cataaaacac taataataat cctgtttaca 300
cgtgactgca gcaggcaggt ccagctccac cactgccctc ctgccacatc acatcaagt 360
ccatggttta gagggttttt catatgtaat tcttttattc tgtaaaagg aacaaaatat 420
acagaacaaa actttccctt tttaaaacta atgttacaaa tctgtattat cacttgata 480
taaatagtat ataagctgat c 501

```

<210> 117

<211> 451

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 320

<223> n = A,T,C or G

<400> 117

```

caagggatat atgttgaggg tacrgrgtga cactgaacag atcacaaagc acgagaaaca 60
ttagttctct ccctccccag cgtctccttc gtctccctgg ttttccgatg tccacagagt 120
gagattgtcc ctaagtaact gcatgatcag agtgctgkct ttataagact cttcattcag 180
cgtatccaat tcagcaattg cttcatcaaa tgccgttttt gccaggctac aggccttttc 240
aggagagttt agaattctcat agtaaaagac tgagaaattt agtgccagac caagacgaat 300

```

```

tggtgtgtgta ggctgcattn ctttcttact aatttcaa at gcttcctggt aagcctgctg 360
ggagttcgac acaagtgggt tgtttgttgc tccagatgcc acttcagaaa gatacctaaa 420
ataatctcct ttcattttca aagtagaaca c 451

```

```

<210> 118
<211> 501
<212> DNA
<213> Homo sapiens

```

```

<400> 118
tccggagccg gggtagtcgc cgccgccgcc gccggtgcag ccaactgcagg caccgctgcc 60
gccgcctgag tagtgggctt aggaaggaag aggtcatctc gtcgggagct tcgctcgga 120
gggtctttgt tccctgcagc cctcccacgg gaatgacaat ggataaaagt gagctggtac 180
agaaagccaa actcgctgag caggctgagc gatatgatga tatggctgca gccatgaagg 240
cagtcacaga acaggggcat gaactctcca acgaagagag aaatctgctc tctgttgct 300
acaagaatgt ggtaaggccg cccgccgctc ttctggcgt gtcactctcca gcattgagca 360
gaaaacagag aggaatgaga agaagcagca gatgggcaaa gaggaccgtg agaagataga 420
ggcagaactg caggacatct gcaatgatgt tctggagctt gttggacaaa tatcttattc 480
caatgctaca caaccagaa a 501

```

```

<210> 119
<211> 391
<212> DNA
<213> Homo sapiens

```

```

<400> 119
aaaaagcagc argttcaaca caaaatagaa atctcaa atg taggatagaa caaaaccaag 60
tgtgtgaggg gggaagcaac agcaaaagga agaaatgaga tgttgcaaaa aagatggagg 120
agggttcccc tctcctctgg ggactgactc aaacactgat gtggcagtat acaccattcc 180
agagtcaggg gtgttcattc ttttttgga gtaagaaaag gtggggatta agaagacgtt 240
tctggaggct tagggaccaa ggctggtctc tttccccct cccaaccccc ttgatccctt 300
tctctgatca ggggaaagga gctcgaatga gggaggtaga gttggaaagg gaaaggattc 360
catttgacag aatgggacag actccttccc a 391

```

```

<210> 120
<211> 421
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 409
<223> n = A,T,C or G

```

```

<400> 120
tggaatagc acagccatcc aggagctctt cargcgcac tcggagcagt tcaactgccat 60
gttccgccgg aaggccttcc tccactggta cacaggcgag ggcatggacg agatggagtt 120
caccgaggct gagagcaaca tgaacgacct cgtctctgag tatcaagcag taccaggatg 180
ccaccgcaga agaggaggag gatttcggtg aggaggccga agaggaggcc taaggcagag 240
cccccatcac cttaggcttc tcagttccct tagccgtctt actcaactgc ccctttctc 300
tccctcagaa tttgtgtttg ctgcctctat cttgtttttt gttttttctt ctgggggggt 360
ctagaacagt gcctggcaca tagtaggcgc tcaataaata cttggttgnt gaatgtctcc 420
t 421

```

```

<210> 121
<211> 206
<212> DNA
<213> Homo sapiens

```

<400> 121
agctggcgct agggctcggt tgtgaaatac agcgtrgtca gcccttgccg tcaagtgtaga 60
aaccacgcc tgtaaggctg gtcttcgtcc atctgctttt ttctgaaata cactaagagc 120
agccacaaaa ctgtaacctc aaggaaacca taaagcttgg agtgccttaa tttttaacca 180
gtttccaata aaacggttta ctacct 206

<210> 122
<211> 131
<212> DNA
<213> Homo sapiens

<400> 122
ggagatgaag atgaggaagc tgagtcagct acgggcargc gggcagctga agatgatgag 60
gatgacgatg tcgataccaa gaagcagaag accgacgagg atgactagac agcaaaaaag 120
gaaaagttaa a 131

<210> 123
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 166, 202, 222, 225
<223> n = A,T,C or G

<400> 123
gatgaaaatt aaataacttaa attaatacaa aggcactacg ataccaccta aaacctactg 60
cctcagtggc agtakgctaa kgaagatcaa gctacagsac atyatcta atgaatgtta 120
gcaattacat akcargaagc atgtttgctt tccagaagac tatggnacaa tggtcattwg 180
ggccaagag gatatttggc cnggaaagga tcaagataga tnaangtaaa g 231

<210> 124
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 284, 412, 513
<223> n = A,T,C or G

<400> 124
gagtagcaac gcaaagcgct tggatttgag tctgtgggsg acttcgggtc cggctctctgc 60
agcagccgtg atcgcttagt ggagtgttta gggtagttgg ccaggatgcc gaatatcaaa 120
atcttcagca ggcagctccc accaggactt atctcasaaa attgctgacc gcctgggcct 180
ggagctaggc aaggtgggtga ctaagaaatt cagcaaccag gagacctgtg tggaaatttg 240
tgaaagtgtg ccgtggagag gatgtctaca ttgttcagag tggntgtggc gaaatcaatg 300
acaatttaat ggagcttttg atcatgatta atgcctgcaa gattgcttca gccagccggg 360
ttactgcagt catcccatgc ttcccttatg ccccggcagg ataagaaaga tnagagccgg 420
gcccgaatc tcagccaagc ttggtgcaaa tatgctatct gtagcagtgc agatcatatt 480
atccacatgc acctacatgc ttctcaaatt canggctttt t 521

<210> 125
<211> 341
<212> DNA
<213> Homo sapiens

<220>
 <221> misc_feature
 <222> 277
 <223> n = A,T,C or G

<400> 125
 atgcaaaagg ggacacaggg ggttcaaaaa taaaaatttc tcttccccct ccccaaacct 60
 gtaccccgagc tccccgacca caacccctt cctcccccg ggaaagcaag aaggagcagg 120
 tgtggcatct gcagctggga agagagaggg cggggagggt ccgagctcgg tgctgggtctc 180
 tttccaaata taaatacgtg tgtcagaact ggaaaatcct ccagcaccca ccaccaagc 240
 actctccgtt ttctgccggt gtttggagag gggcgnggg caggggcgcc aggcaccggc 300
 tggctgcggt ctactgcatc cgctgggtgt gcaccccgcg a 341

<210> 126
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 353, 399, 455
 <223> n = A,T,C or G

<400> 126
 aggttggaga aggtcatgca ggtgcagatt gtccaggskc agccacaggg tcaagcccaa 60
 caggcccaga gtggcactgg acagaccatg caggtgatgc agcagatcat cactaacaca 120
 ggagagatcc agcagatccc ggtgcagctg aatgccggcc agctgcagta tatccgctta 180
 gccagcctg tatcaggcac tcaagttgtg cagggacaga tccagacact tgccaccaat 240
 gctcaacaga ttacacagac agaggtccag caaggacagc agcagttcaa gccagttcac 300
 aagatggaca gcagctctac cagatccagc aagtcacat gcctgcgggc cangacctcg 360
 ccagcccatg ttcatccagt caagccaacc agcccttcna cgggcaggcc ccccagggtga 420
 ccggcgactg aagggcctga gctggcaagg ccaangacac ccaacacaat ttttgccata 480
 cagcccccag gcaatgggca cagcctttct tcccagagga c 521

<210> 127
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 127
 tgagatttat tgcatttcat gcagcttgaa gtccatgcaa aggrgactag cacagttttt 60
 aatgcattta aaaaataaaa gggagggtggg cagcaaacac acaaagtcct agtttcctgg 120
 gtccctggga gaaaagagtg tggcaatgaa tccaccact ctccacaggg aataaatctg 180
 tctcttaaata gcaaagaatg tttccatggc ctctggatgc aaatacacag agctctgggg 240
 tcagagcaag ggatggggag aggaccacga gtgaaaaagc agctacacac attcacctaa 300
 ttccatctga gggcaagaac aacgtggcaa gtcttggggg tagcagctgt t 351

<210> 128
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 128
 tccagacatg ctctgtcct aggcggggag caggaaccag acctgctatg ggaagcagaa 60
 agagttaagg gaaggtttcc ttctattcct gttccttctc ttttgctttt gaacagtttt 120
 taaatatact aatagctaag tcatttgcca gccagggtccc ggtgaacagt agagaacaag 180
 gagcttgcta agaattaatt ttgctgtttt tcacccatt caaacagagc tgccctgttc 240

```

cctgatggag ttccattcct gccagggcac ggctgagtaa cacgaagcca ttcaagaaaag 300
gcggggtgtga aatcactgcc accccatgga cagaccctc actcttcctt cttagccgca 360
gcgctactta ataaatata ttatactttg aaattatgat aaccgatttt tcccatgcgg 420
catcctaagg gcacttgcca gctcttatcc ggacagtcaa gcactgttgt tggacaacag 480
ataaaggaaa agaaaaagaa gaaaacaacc gcaacttctg t 521

```

<210> 129

<211> 521

<212> DNA

<213> Homo sapiens

<400> 129

```

tgagacggac cactggcctg gtccccctc atktgctgtc gtaggacctg acatgaaacg 60
cagatctagt ggcagagagg aagatgatga ggaacttctg agacgtcggc agcttcaaga 120
agagcaatta atgaagctta actcaggcct gggacagtgt atcttgaaag aagagatgga 180
gaaagagagc cgggaaaggt catctctgtt agccagtgcg tacgattctc ccatcaactc 240
agcttcacat attccatcat ctaaaactgc atctctccct ggctatggaa gaaatgggct 300
tcaccggcct gtttctaccg acttcgctca gtataacagc tatggggatg tcagcggggg 360
agtgcgagat taccagacac ttccagatgg ccacatgcct gcaatgagaa tggaccgagg 420
agtgtctatg cccaacatgt tggaaccaa gatatttcca tatgaaatgc tcatggtgac 480
caacagaggg ccgaaaccaa atctcagaga ggtggacaga a 521

```

<210> 130

<211> 270

<212> DNA

<213> Homo sapiens

<400> 130

```

tcactttatt tttcttgat aaaaacccta tgttgtagcc acagctggag cctgagtccg 60
ctgcacggag actctggtgt gggctctgac gaggtggtca gtgaactcct gatagggaga 120
cttggtgaat acagtctcct tccagaggtc gggggtcagg tagctgtagg tcttagaaat 180
ggcatcaaag gtggccttgg cgaagttgcc caggggtggca gtgcagcccc gggctgaggt 240
gtagcagtca tcgataccag ccatcatgag
270

```

<210> 131

<211> 341

<212> DNA

<213> Homo sapiens

<400> 131

```

ctggaatata gaccctgat cgacaaaact ttgaacgagg ctgactgtgc caccgtcccg 60
ccagccattc gctcctactg atgagacaag atgtggtgat gacagaatca gcttttgtaa 120
ttatgtataa tagctcatgc atgtgtccat gtcataactg tcttcatacg cttctgact 180
ctggggaaga aggagtacat tgaagggaga ttggcaccta gtggctggga gcttgccagg 240
aaccagtggt ccaggagcgt tggcacttac ctttgtccct tgcttcattc ttgtgagatg 300
ataaaactgg gcacagctct taaataaaat ataatgaac a 341

```

<210> 132

<211> 844

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 37

<223> n = A,T,C or G

<400> 132

```

tgaatgggga ggagctgacc caggaaatgg agcttgngga gaccaggcct gcaggggatg 60
gaaccttcca gaagtgggca tctgtggtgg tgccctcttg gaaggagcag aagtacacat 120
gccatgtgga acatgagggg ctgcctgagc ccctcaccct gagatggggc aaggaggagc 180
ctccttcac caccaagact aacacagtaa tcattgctgt tccggttgtc cttggagctg 240
tggtcatcct tggagctgtg atggcttttg tgatgaagag gaggagaaac acaggtggaa 300
aaggagggga ctatgctctg gctccaggct ccagagctc tgatatgtct ctccagatt 360
gtaaagtgtg aagacagctg cctggtgtgg acttgggtgac agacaatgtc ttcacacatc 420
tcctgtgaca tccagagacc tcagttctct ttagtcaagt gtctgatgtt ccctgtgagt 480
ctgctgggctc aaagtgaaga actgtggagc ccagtccacc cctgcacacc aggaccctat 540
ccctgcactg ccctgtgttc ccttccacag ccaaccttgc tgctccagcc aaacatttgt 600
ggacatctgc agcctgtcag ctccatgcta ccctgacctt caactcctca cttccacact 660
gagaataata atttgaatgt ggggtggctgg agagatggct cagcgctgac tgctcttcca 720
aaggctcctga gttcaaatcc cagcaaccac atgggtggctc acaaccatct gtaatgggat 780
ctaataccct cttctgcagt gtctgaagac asctacagtg tacttacata taataataaa 840
taag 844

```

<210> 133

<211> 601

<212> DNA

<213> Homo sapiens

<400> 133

```

ggccggggcgc gcgcgcccc gccacacgca cgccggggcgt gccagtttat aaagggagag 60
agcaagcagc gagtcttgaa gctctgtttg gtgcttttga tccatttcca tcggtcctta 120
cagccgctcg tcagactcca gcagccaaga tgggtgaagca gatcgagagc aagactgctt 180
ttcaggaagc cttggacgct gcaggtgata aacttgtagt agttgacttc tcagccacgt 240
gggtgtgggcc ttgcaaaatg atcaagcctt tctttcattc cctctctgaa aagtattcca 300
acgtgatatt ccttgaagta gatgtggatg actgtcagga tgttgcttca gagtgtgaag 360
tcaaattgcat gccaacattc cagtttttta agaagggaca aaaggtgggt gaattttctg 420
gagccaataa ggaaaagctt gaagccacca ttaatgaatt agtctaataca tgttttctga 480
aaatataacc agccattggc tatttaaaac ttgtaatttt ttaattttac aaaaatataa 540
aatatgaaga cataaaccm gttgccatct gcgtgacaat aaaacattaa tgctaacact 600
t 601

```

<210> 134

<211> 421

<212> DNA

<213> Homo sapiens

<400> 134

```

tcacataaga aatttaagca agttacrcta tcttaaaaaa cacaacgaat gcattttaat 60
agagaaaccc ttccctccct ccacctccct cccccaccct cctcatgaat taagaatcta 120
agagaagaag taaccataaa accaagtttt gtggaatcca tcatccagag tgcttacatg 180
gtgattaggt taatattgcc ttcttataaa atttctatct taaaaaaaat tataaccttg 240
attgcttatt acaaaaaaat tcagtacaaa agttcaatat attgaaaaat gcttttcccc 300
tccctcacag caccgtttta tatatagcag agaataatga agagattgct agtctagatg 360
gggcaatctt caaattacac caagacgcac agtggtttat ttaccctccc cttctcataa 420
g 421

```

<210> 135

<211> 511

<212> DNA

<213> Homo sapiens

<400> 135

```

ggaaaggatt caagaattag aggacttgct tgctrragaa aaagacaact ctctgcgcat 60
gctgacagac aaagagagag agatggcgga aataagggat caaatgcagc aacagctgaa 120
tgactatgaa cagcttcttg atgtaaagtt agccctggac atggaaatca gtgcttacag 180

```

```

gaaactctta gaaggcgaag aagagaggtt gaagctgtct ccaagccctt cttcccgtgt 240
gacagtatcc cgagcatcct caagtcgtag tgtaccgtac aactagagga aagcggaaga 300
gggttgatgt ggaagaatca gaggcgaagt agtagtgta gcatctctca ttccgcctca 360
accactggaa atgtttgcat cgaagaaatt gatgttgatg ggaaatttat cccgcttgaa 420
gaacacttct gaacaggatc aaccaatggg aaggcttggg agatgatcag aaaaattgga 480
gacacatcag tcagttataa atataacctca a                                     511

```

<210> 136

<211> 341

<212> DNA

<213> Homo sapiens

<400> 136

```

catgggtttc accaggtttg ccaggctgct cttgaactsc tgacctcagg tgatccaccc 60
gcctcggcct cccaaagtgc tgggattaca ggcgtgagcc accacgcccg gccccaaaag 120
ctgtttcttt tgtcttttagc gtaaagctct cctgccatgc agtatctaca taactgacgt 180
gactgccagc aagctcagtc actcogtggg ctttttctct ttccagttct tctctctctc 240
ttcaagttct gcctcagtg aagctgcagg tccccagtta agtgatcagg tgagggttct 300
ttgaacctgg ttctatcagt cgaattaatc cttcatgatg g                                     341

```

<210> 137

<211> 551

<212> DNA

<213> Homo sapiens

<400> 137

```

gatgtgttg accctctgtg tcaaaaaaaaa cctcacaaag aatcccctgc tcattacaga 60
agaagatgca tttaaaatat gggttatttt caacttttta tctgaggaca agtatccatt 120
aattattgtg tcagaagaga ttgaatacct gcttaagaag cttacagaag ctatgggagg 180
aggttggcag caagaacaat ttgaacatta taaaatcaac tttgatgaca gtaaaaatgg 240
cctttctgca tgggaactta ttgagcttat tggaaatgga cagtttagca aaggcatgga 300
ccggcagact gtgtctatgg caattaatga agtctttaat gaacttatat tagatgtgtt 360
aaagcagggt tacatgatga aaaagggcca cagacggaaa aactggactg aaagatgggt 420
tgtactaaaa cccaacataa tttcttacta tgtgagtga gatctgaagg ataagaaagg 480
agacattctc ttggatgaaa attgctgtgt agaagtcctt gcctgacaaa agatggaaaag 540
aatgccttt t                                     551

```

<210> 138

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 490

<223> n = A,T,C or G

<400> 138

```

gactggttct ttatttcaaa aagacacttg tcaatattca gtrtcaaaac agttgcacta 60
ttgatttctc tttctcccaa tcggccccaa agagaccaca taaaaggaga gtacatttta 120
agccaataag ctgcaggatg tacacctaac agacctccta gaaaccttac cagaaaatgg 180
ggactgggta gggaaggaaa cttaaaagat caacaaactg ccagcccacg gactgcagag 240
gctgtcacag ccagatgggg tggccagggt gccacaaacc caaagcaaag tttcaaaata 300
atataaaatt taaaaagttt tgtacataag ctattcaaga tttctccagc actgactgat 360
acaaagcaca attgatgg cacttctaga gacagcagct tcaaaccag aaaaggggtga 420
tgagatgaag tttcacatgg ctaaatcagt ggcaaaaaca cagtcttctt tctttcttc 480
tttcaaggan gcaggaaaagc aattaagtgg tcaccttaac ataaggggga c                                     531

```

<210> 139
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 517
 <223> n = A,T,C or G

```
<400> 139
tgggtgggca ccatggctgg gatcaccacc atcgaggcgg tgaagcgcaa gatccaggtt 60
ctgcagcagc aggcagatga tgcagaggag cgagctgagc gcctccagcg agaagttgag 120
ggagaaaaggc gggcccggga acaggctgag gctgagggtg cctccttgaa ccgtaggatac 180
cagctggttg aagaagagct ggaccgtgct caggagcgcc tggccactgc cctgcaaaag 240
ctggaagaag ctgaaaaagc tgctgatgag agtgagagag gtatgaaggt tattgaaaac 300
cgggccttaa aagatgaaga aaagatggaa ctccaggaaa tccaactcaa agaagctaag 360
cacattgcag aagaggcaga taggaagtat gaagagggtg ctcgtaagtt ggtgatcatt 420
gaaggagact tggaaaccga cagaaggaac gagcttgagc ttggcaaaaag tcccgttgcc 480
cagagatggg atgaaccaga ttagactgat ggaccanaac c 521
```

<210> 140
 <211> 571
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 7
 <223> n = A,T,C or G

```
<400> 140
aggggcngcg ggtgcgtggg ccaactgggtg accgaacttag cctggccaga ctctcagcac 60
ctggaagcgc cccgagagtg acagcgtgag gctgggaggg aggacttggc ttgagcttgt 120
taaacctctgc tctgagcctc cttgtgcct gcatttagat ggctcccgca aagaaggggtg 180
gcgagaagaa aaagggccgt tctgccatca acgaagtggg aacccgagaa tacaccatca 240
acattcacaa gcgcattccat ggagtgggct tcaagaagcg tgcacctcgg gcaactcaaag 300
agattcggaa atttgccatg aaggagatgg gaactccaga tgtgcgcatt gacaccaggc 360
tcaacaaagc tgtctgggccc aaaggaataa ggaatgtgcc ataccgaatc cgggtgtgcgg 420
ctgtccagaa aacgtaatga ggatgaagat tcaccaaata agctatatac tttggttacc 480
tatgtacctg ttaccacttt caaaaatcta cagacagtca atgtggatga gaactaatcg 540
ctgatcgta gatcaataa agttataaaa t 571
```

<210> 141
 <211> 531
 <212> DNA
 <213> Homo sapiens

```
<400> 141
tcgggagcca cacttggccc tcttcctctc caaagsgcca gaacctcctt ctctttggag 60
aatggggagg cctcttgagg acacagaggg tttcaccttg gatgacctct agagaaattg 120
ccaagaagc ccaccttctg gtcccaacct gcagaccca cagcagtcag ttggtcaggc 180
cctgctgtag aaggtcactt ggctccattg cctgcttcca accaatgggc aggagagaag 240
gcctttatct ctcgcccacc catctctcct gtaccagcac ctccggtttc agtcagtgtt 300
gtccagcaac ggtaccgttt acacagtcac ctcagacaca ccatttcacc tcccttgcca 360
agctgttagc cttagagtga ttgcagtga cactgtttac acaccgtgaa tcoattccca 420
tcagtcatt ccagttggca ccagcctgaa ccatttggtt cctgggtgta actggagtcc 480
tgtttacaag gtggagtcgg ggcttgctga cttctcttca tttgagggca c 531
```

<210> 142
<211> 491
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 410
<223> n = A,T,C or G

<400> 142
acctagacag aaggtgggtg agggaggact ggtaggaggc tgaggcaatt ccttggtagt 60
ttgtcctgaa accctactgg agaagtcagc atgaggcacc tactgagaga agtgcccaga 120
aactgctgac tgcattctgtt aagagttaac agtaaagagg tagaagtgtg tttctgaatc 180
agagtggaag cgtctcaagg gtcccacagt ggaggtccct gagctacctc ccttccgtga 240
gtgggaagag tgaagcccat gaagaactga gatgaagcaa ggatgggggt cctgggctcc 300
aggcaagggc tgtgtctctc gcagcaggga gccccacgag tcagaagaaa agaactaatc 360
atthgttgca agaaaccttg cccggatact agcggaaaac tggaggcggn ggtgggggca 420
caggaaagtg gaagtgattt gatggagagc agagaagcct atgcacagtg gccgagtcga 480
cttgtaaagt g 491

<210> 143
<211> 515
<212> DNA
<213> Homo sapiens

<400> 143
ttcaagcaat tgtaacaagt atatgtagat tagagtgagc aaaatcatat acaattttca 60
tttccagttg ctattttcca aattgttctg taatgtcgtt aaaattactt aaaaattaac 120
aaagccaaaa attatattta tgacaagaaa gccatcccta cattaatctt acttttccac 180
tcaccggccc atctccttcc tctttttcct aactatgcca ttaaaactgt tctactgggc 240
cgggcggtgt gctcatgcct gtaatcccag cattttggga ggccaaggca ggcggtatcat 300
gaggtcaaga gattgagacc atcctggcca acatggtgaa accccgcctc gactaagaat 360
acaaaaatta gctgggcatg gtggcgcatg cctgtagtct cagctactcg ggaggctgag 420
gcagaagaat cgcttgaacc cgggaggcag aggatgcagt gagccccgat cgcgccactg 480
cactctagcc tgggcgacag actgagactc tgctc 515

<210> 144
<211> 340
<212> DNA
<213> Homo sapiens

<400> 144
tgtgccagtc tacaggccta tcagcagcga ctcttcagc aacagatggg gtcccctgtt 60
cagcccaacc ccatgagccc ccagcagcat atgctcccaa atcaggccca gtcccacac 120
ctacaaggcc agcagatccc taattctctc tccaatcaag tgcgtctctc ccagcctgtc 180
ccttctccac ggccacagtc ccagccccc cactccagtc cttccccaag gatgcagcct 240
cagccttctc cacaccagtc ttccccacag acaagttccc cacatcctgg actggtagt 300
gccagggcca accccatgga acaagggcct tttgccagcc 340

<210> 145
<211> 630
<212> DNA
<213> Homo sapiens

<400> 145
tgtaaaaact tgthtttaatt tttgtataaa ataaagggtg tccatgccca cgggggctgt 60

```

aggaaatcca agcagaccag ctgggggtggg gggatgtagc ctacctcggg ggactgtctg 120
tcctcaaaac gggctgagaa ggcccgtcag gggcccaggt cccacagaga ggcctgggat 180
actcccccaa cccgaggggc agactgggca gtggggagcc cccatcgtgc cccagaggtg 240
gccacaggct gaaggagggg cctgaggcac cgcagcctgc aacccccagg gctgcagtcc 300
actaactttt tacagaataa aaggaacatg gggatgggga aaaaagcacc aggtcaggca 360
gggcccagag gcccagatc ccaggagggc caggactcag gatgccagca ccaccctagc 420
agctcccaca gctcctggca caggaggccg ccacggattg gcacaggccg ctgctggcca 480
tcacgccaca tttggagaac ttgtcccagc agaggtcagc tcggaggagc tcctcgtggg 540
cacacactgt acgaacacag atctccttgt taatgacgta cacacggcgg aggctgcggg 600
gacagggcac gggaggtctc agccccactt

```

<210> 146

<211> 521

<212> DNA

<213> Homo sapiens

<400> 146

```

atggctgctg gatttaggtg gtaatagggg ctgtggggcca taaatctgaa gccttgagaa 60
ccttgggtct ggagagccat gaagaggga ggaagagagg gcaagtcctg aacctaacca 120
atgacctgat ggattgctcg accaagacac agaagtgaag tctgtgtctg tgcacttccc 180
acagactgga gtttttggtg ctgaatagag ccagttgcta aaaaattggg ggtttggtga 240
agaaatctga ttgttgtgtg tattcaatgt gtgattttta aaataaacag caacaacaat 300
aaaaaccctg actggctgtt ttttcctgt attctttaca actatTTTTT gaccctctga 360
aaattattat acttcaccta aatggaagac tgctgtgttt gtggaaattt tgtaattttt 420
taatttattt tattctctct cctttttatt ttgcctgcag aatccgttga gagactaata 480
aggcttaata ttttaattgat ttgtttaata tgtatataaa t 521

```

<210> 147

<211> 562

<212> DNA

<213> Homo sapiens

<400> 147

```

ggcatgcgag cgcactcggc ggacgcaagg gcggcgggga gcacacggag cactgcaggc 60
gccgggttgg gacagcgtct tcgctgctgc tggatagtcg tgttttcggg gatcgaggat 120
actcaccaga aaccgaaaat gccgaaacca atcaatgtcc gagttaccac catggatgca 180
gagctggagt ttgcaatcca gccaaataca actggaaaac agctttttga tcagggtgga 240
aagactatcg gcctccggga agtggtgtac tttggcctcc actatgtgga taataaagga 300
tttcctacct ggctgaagct ggataagaag gtgtctgccc aggaggtcag gaaggagaat 360
cccctccagt tcaagttccg ggccaaagtt ctaccctgaa gatgtggctg aggagctcat 420
ccaggacatc acccagaaac ttttcttcct tcaagtgaag gaaggaatcc ttagcgatga 480
gatctactgc cccccttgar actgccgtgc tcttgggggc ctacgcttgt gcatgccaa 540
tttggggact accaccaaga ag

```

<210> 148

<211> 820

<212> DNA

<213> Homo sapiens

<400> 148

```

gaaggagtgc ggatactcag cattgatgca ccccaatttc aaagcggcat tcttcggcag 60
gtctctggga caatctctag ggtcactacc tggaaactcg ttagggatca actgaatgct 120
gaaaggaaaag aacacctgca gaaccggaca gaaattcacc ccggcgatca gctgattgat 180
ctcggctcgac cagaagtcac ggctaaagat gacgaggacg ttgtcaattc cctgggcttt 240
tcgaagttag tccagcagca gtctgaggta ttcgggccgg ttatgcacct ggaccaccag 300
caccagctcc cgggggggccc aggtgccagc cttatctaca ttctcaggg tctgatcaaa 360
gttcagctgg tacaccaggg accggtaccg cagcgtcagg ttgtccgctc gggctggggg 420
accgccggga ccagggaagc cgccgacacg ttggagacce tgcggatgcc cacagccaca 480

```

```

gaggggtggt cccacccgcg gccgcggcga cccgcgcgcg gttcggcgctc cagcaacgggt 540
ggggcgaggg cctcggttctt cctttgtcgc ccattgctgc tccagaggac gaagccgcag 600
gcggccacca cgagcgtcag gattagcacc ttccggttgt agatgcggaa cctcatggtc 660
tccagggccg ggagcgcagc tacagctcga gcgtcggcgc cgccgctagg agcccgggct 720
cggcttcgtc tccgtcctct ccattcagca ccacgggtcc cggaaaaagc tcagccscgg 780
tcccaaccgc accctagctt cgttacctgc gcctcgcttg 820

```

<210> 149

<211> 501

<212> DNA

<213> Homo sapiens

<400> 149

```

cagattttta tttgcagtcg tcaactggggc cgtttcttgc tgcttatttg tctgctagcc 60
tgctcttcca gctgcatggc caggcgcaag gccttgatga catctcgag ggctgagaaa 120
tgcttggtct gctgggcccag agcagattcc gctttgttca caaaggctct caggtcatag 180
tctggctgct cggtcatctc agagagctca agccagctct gtccttgctg tatgatctcc 240
ttgagctctt ccatagcctt ctctccagc tccctgatct gagtcatggc ttcgttaaag 300
ctggacatct gggaagacag ttctctctct tccttgata aattgcctgg aatcagcgcc 360
ccgttagagc aggccttccat ctcttctgtt tccatttgaa tcaactgctc tccactgggc 420
ccactgtggg ggctcagctc cttgaccctg ctgcatact taagggtgtt taaaggatat 480
tcacaggagc ttatgcctgg t 501

```

<210> 150

<211> 511

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 457, 479

<223> n = A,T,C or G

<400> 150

```

ctctcttgg tacatgaacc caagttgaaa gtggacttaa caaagtatct ggagaaccaa 60
gcattctgct ttgactttgc atttgatgaa acagcttcga atgaagttgt ctacagggttc 120
acagcaaggc cactggtaca gacaatcttt gaagggtgaa aagcaacttg tttgcatat 180
ggccagacag gaagtggcaa gacacatact atgggcggag acctctctgg gaaagcccag 240
aatgcatcca aagggatcta tgccatggcc ttccgggacg tcttctctctg aagaatcaac 300
cctgctaccg gaagttgggc ctggaagtct atgtgacatt cttcgagatc tacaatggga 360
agctgtttga cctgtcaac aagaaggcca agcttgcgcg tgctggaaga cggcaagcaa 420
caggtgcaag tgggtggggc ttgcaggaac atctggntaa ctctgcttga tgatggcant 480
caagatgata gacatgggca gcgcctgcag a 511

```

<210> 151

<211> 566

<212> DNA

<213> Homo sapiens

<400> 151

```

tcccgaattc aagcgacaaa ttggawagtg aaatggaaga tgcctatcat gaacatcagg 60
caaatctttt gcgccaagat ctgatgagac gacaggaaga attaagacgc atggaagaac 120
ttcacaatca agaaatgcag aaacgtaaag aaatgcaatt gaggcaagag gaggaacgac 180
gtagaagaga ggaagagatg atgattcgct aacgtgagat ggaagaacaa atgagggcgc 240
aaagagagga aagttacagc cgaatgggct acatggatcc acgggaaaga gacatgcgaa 300
tgggtggcgg aggagcaatg aacatgggag atccctatgg ttcaggaggc cagaaatttc 360
cacctctagg aggtggtggt ggcatagggt atgaagctaa tcctggcggt ccaccagcaa 420
ccatgagtgg ttccatgatg ggaagtgaca tgcgtactga gcgctttggg cagggaggtg 480

```

cggggcctgt ggggtggacag ggtcctagag gaatggggcc tggaactcca gcaggatatg 540
 gtagagggag agaagagtac gaaggc 566

<210> 152

<211> 518

<212> DNA

<213> Homo sapiens

<400> 152

ttcgtgaaga ccctgactgg taagaccatc actctcgaag tggagcccga gtgacaccat 60
 tgagaatgtc aaggcaaaga tccaagacaa ggaaggcatc cctcctgacc agcakagggtt 120
 gatcctttgtc gggaaacagc tggaagatgg acgcaccctg tctgactaca acatccagaa 180
 agagtccacc ctgcacctgg tgctccgtct cagaggtggg atgcaaactc tctgtgaagac 240
 cctgactggg aagaccatca ccctcgaggt ggagcccagt gacaccatcg agaattgtcaa 300
 ggcaaagatc caagataagg aaggcatccc tcctgatcag cagaggttga tctttgctgg 360
 gaaacagctg gaagatggac gcacctgtc tgactacaac atccagaaag agtccactct 420
 gcacttggtc ctgcgcttga ggggggggtg ctaagtttcc ctttttaagg tttcaacaaa 480
 tttcattgca ctttcctttc aataaagttg ttgcatte 518

<210> 153

<211> 542

<212> DNA

<213> Homo sapiens

<400> 153

gcgcgggtgc gtggggcact gggtgaccga cttagcctgg ccagactctc agcacctgga 60
 agcgccccga gactgacagc gtgaggctgg gagggaggac ttggcttgag ctgtttaaac 120
 tctgctctga gcctccttgt cgcctgcatt tagatggctc ccgcaaagaa gggtgggcag 180
 aagaaaaagg gccgttctgc catcaacgaa gtggttaacc gagaaatacac catcaacatt 240
 cacaagcgca tccatggagt gggcttcaag aagcgtgcac ctggggcact caaagagatt 300
 cggaaatttg ccatgaagga gatgggaact ccagatgtgc gcattgacac caggctcaac 360
 aaagctgtct gggccaaagg aataaggaat gtgccatacc gaatccgtgt gcggctgtcc 420
 agaaaacgta atgaggatga agattcacca aataagctat atacttttgt tacctatgta 480
 cctgttacca ctttcaaaaa tctacagaca gtcaatgtgg atgagaacta atcgtctgac 540
 gt 542

<210> 154

<211> 411

<212> DNA

<213> Homo sapiens

<400> 154

aattctttat ttaaataaac aaactcatct tcctcaagcc ccagaccatg gtaggcagcc 60
 ctccctctcc atccctcac cccacccctt agccacagtg aagggaatgg aaaatgagaa 120
 gccacgaggg ccctgccag ggaaggctgc ccagatgtg tggtagcac agtcagtgc 180
 gctgtggctg gggcagcagc tgccacaggc tcctccctat aaattaagtt cctgcagcca 240
 cagctgtggg agaagcatac ttgtagaagc aaggccagtc cagcatcaga aggcagaggc 300
 agcatcagt actcccagcc atggaatgaa cggaggacac agagctcaga gacagaacag 360
 gccaggggga agaaggagag acagaatagg ccagggcatg gcggtgaggg a 411

<210> 155

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 173

<223> n = A,T,C or G

<400> 155

```

tgatgaatct ggggtgggctg gcagtagccc gagatgatgg gctcttctct ggggatccca 60
actgggtccc taagaaatcc aaggagaatc ctcggaactt ctcggaatac cagctgcaag 120
agggcaagaa cgtgatcggg ttacagatgg gcaccaaccg cggggcgctc cangcaggca 180
tgactggcta cgggatgcc a gccagatcc tctgatccca cccaggcct tgcccctgcc 240
ctcccacgaa tggttaatat atatgtagat atatatatta gcagtgcacat tcccagagag 300
cccagagct ctcaagctcc tttctgtcag ggtggggggg tcaagcctgt cctgtcacct 360
ctgaagtgcc tgctggcatc ctctcccca tgcttactaa tacattccct tcccatagac 420
c 421

```

<210> 156

<211> 670

<212> DNA

<213> Homo sapiens

<400> 156

```

agcggagctc cctcccctgg tggttacaac ccacacacgc caggctcagg catcgagcag 60
aactccagcg actgggtaac cactgacatt cagggtgaagg tgcgggacac ctacctggat 120
acacaggtgg tgggacagac aggtgtcatc cgcagtgta cggggggcat gtgctctgtg 180
tacctgaagg acagtgaagaa ggttgtcagc atttccagtg agcacctgga gcctatcacc 240
bccaccaaga acaacaaggt gaaagtgatc ctgggcgagg atcggaagc cacgggcgtc 300
ctactgagca ttgatgggta ggatggcatt gtccgtatgg accttgatga gcagctcaag 360
atcctcaacc tccgcttcct ggggaagctc ctggaagcct gaagcaggca gggccgggtg 420
acttcgtcgg atgaagagt atcctccttc cttccctggc ccttggctgt gacacaagat 480
cctcctgcag ggctaggcgg attgttctgg atttcccttt gtttttcctt ttaggtttcc 540
atcttttccc tccctgggtc tcattggaat ctgagtagag tctgggggag ggtccccacc 600
ttcctgtacc tcctccccc acgttgcttt tgttgtaccg tctttcaata aaaagaagct 660
gtttggtcta 670

```

<210> 157

<211> 421

<212> DNA

<213> Homo sapiens

<400> 157

```

ggttcacagc actgctgctt gtgtgttgcc ggccaggaat tccaggctca caaggctatc 60
ttagcagctc gttctccggt ttttagtgcc atgtttgaac atgaaatgga ggagagcaaa 120
aagaatcgag ttgaaatcaa tgatgtggag cctgaagttt ttaaggaaat gatgtgcttc 180
atttacacgg ggaaggctcc aaacctcgac aaaatggctg atgatttgct ggcagctgct 240
gacaagtatg ccctggagcg cttaaaggct atgtgtgagg atgccctctg cagtaacctg 300
tccgtggaga acgtgcaga aattctcatc ctggccgacc tccacagtgc agatcagttg 360
aaaactcagg cagtggattt catcaactat catgcttcgg atgtcttgga gacctcttgg 420
g 421

```

<210> 158

<211> 321

<212> DNA

<213> Homo sapiens

<400> 158

```

tcgtagccat ttttctgctt ctttggagaa tgacgccaca ctgactgctc attgtcgttg 60
gttccatgcc aattgggtgaa atagaacctc atccggtagt ggagccggag ggacatcttg 120
tcatcaacgg tgatgggtgcg atttggagca taccagagct tgggtgttctc gccatacagg 180
gcaaagaggt tgtgacaaa aggagagata cggcatgcct gtgcagccct gatgcacagt 240
tcctctgctg tgtactctcc actgccagc cgagggggct ccctgtccga cagatagaag 300
atcacttcca ccctggctt g 321

```

<210> 159
 <211> 596
 <212> DNA
 <213> Homo sapiens

<400> 159
 tggcacactg ctcttaagaa actatgawga tctgagattt ttttgtgtat gtttttgact 60
 cttttgagtg gtaatcatat gtgtctttat agatgtacat acctccttgc acaaattggag 120
 ggggaattcat tttcatcact gggagtggtcc ttagtgata aaaaccatgc tggatatatg 180
 cttcaagttg taaaaatgaa agtgacttta aaagaaaata ggggatggtc caggatctcc 240
 actgataaga ctgttttttaa gtaacttaag gacctttggg tctacaagta tatgtgaaaa 300
 aaatgagact tactgggtga ggaaattcat tgtttaaaga tggtcgtgtg tgtgtgtgtg 360
 tgtgtgtgtg ttgtgtgtgt ttttgttttt taaggagggy aatttattat ttaccgttgc 420
 ttgaaattac tgkgtaaata tatgtytgat aatgatttgc tytttgvcm aaaaaattag 480
 gvctgtataa gtwctaratg cmtccctggg kgttgatyt ccmagatatt gatgatamcc 540
 cttaaaattg taaccygcct ttttcccttt gctytcmtt aaagtctatt cmaaag 596

<210> 160
 <211> 515
 <212> DNA
 <213> Homo sapiens

<400> 160
 gggggtaggc tctttattag acggttattg ctgtactaca gggtcagagt gcagtgtgag 60
 cagtgtcaga ggccgcggt cagcccaaga atgtggattt tctctcccta ttgatcacag 120
 tgggtgggtt tcttcagaaa agccccagag gcagggacca gtgagctcca aggttagaag 180
 tggaactgga aggccttcagt cacatgctgc ttccacgctt ccaggctggg cagcaaggag 240
 gagatgccca tgacgtgccca ggtctcccca tctgacacca gtgaagtctg gtaggacagc 300
 agccgcacgc ctgcctctgc caggaggcca atcatggtag gcagcattgc agggtcagag 360
 gtctgagtc ggaataggag caggggcagg tcctgcgga gaggcacttc tggcctgaag 420
 acagctccat tgagcccctg cagtacaggy gtagtgcctt ggaccaagcc cacagcctgg 480
 taaggggagc ctgccagggc cagggccagg aggca 515

<210> 161
 <211> 936
 <212> DNA
 <213> Homo sapiens

<400> 161
 taatttctta gtcgttttga atccttaagc atgcaaaagc tttgaacaga agggttcaca 60
 aaggaaccag ggttgtctta tggcatccag ttaagccaga gctgggaatg cctctgggtc 120
 atccacatca ggagcagaag cacttgactt gtcggtcctg ctgccacggt ttgggcgccc 180
 accacgcca cgtccacctc gtcctccctt gccgccagc cctgggcggc caaggtctcc 240
 aaaattgatc tcagctgag acgttatatc atttgcgtgc ttccggaaat gatggtccat 300
 aaccgaatct tcagcatgag cctcttcaact ctttgattta tgaagaacaa atcccttctt 360
 ccactgcca tcagcacctt catattggtt tggatatta aattctactt ttgccgggtc 420
 cttattttga atagccttcc actcatccaa agtcatctct tttggaccct cctcttttac 480
 ctcttcaact tcattctcct tattttcagt gtctgccact ggatgatgtt cttcaccttc 540
 aggtgtttcc tcagtcacat ttgattgatc caagtcagtt aattcgtctt tgacagttcc 600
 ccagttgtga gatccgtac ctccacgttt gtcctcgtgc ttcaggccag atctatcact 660
 tccactatgc ctatcaaatt cacgtttgcc acgagaatca aatccatctc ctccgcccac 720
 tccacgtcca cgccccctc gacctcttcc aagaccacca cgacctcgaa taggtcggtc 780
 aataatcggg ctatcaactg aaaattcgcc tccttcaccc ttttcttcaa gtggcctttc 840
 gaatcttcgt tcacgaggtg gtcgccttct tggctctcta tcaattattt tcccttcacc 900
 ctgaagttgt tgatcaggtc ttcttccaac tcgtgc 936

<210> 162

<211> 950
<212> DNA
<213> Homo sapiens

<400> 162
aagcggatgg acctgagtca gccgaatcct agcccccctcc cttgggcctg ctgtgggtgct 60
cgacatcagt gacagacgga agcagcagac catcaaggct acgggaggcc cggggcgctt 120
gcgaagatga agtttggtg cctctccttc cggcagcctt atgctggctt tgtcttaaatt 180
ggaatcaaga ctgtggagac gcgctggcgt cctctgctga gcagccagcg gaactgtacc 240
atcgccgtcc acattgctca cagggactgg gaaggcgatg cctgtcggga gctgctgggtg 300
gagagactcg ggatgactcc tgctcagatt caggccttgc tcaggaaagg ggaaaagttt 360
ggtcgaggag tgatagcggg actcgttgac attggggaaa ctttgcaatg cccgaagac 420
ttaactcccg atgagggtgt ggaactagaa aatcaagctg cactgaccaa cctgaagcag 480
aagtacctga ctgtgatttc aaacccagg tggttactgg agcccatacc taggaaagga 540
ggcaaggatg tattccaggt agacatccca gagcacctga tccctttggg gcatgaagtg 600
tgacaagtgt gggctcctga aaggaatgtt ccrgagaaac cagctaaatc atggcacctt 660
caatttgcca tcgtgacgca gacctgtata aattagggtta aagatgaatt tccactgctt 720
tggagagtcc caccactaa gcaactgtgca tgtaaacagg ttcctttgct cagatgaagg 780
aagtaggggg tggggctttc cttgtgtgat gcctccttag gcacacaggc aatgtctcaa 840
gtactttgac cttagggtag aaggcaaaag tgccagtaaa tgtctcagca ttgctgctaa 900
ttttggtcct gctagtttct ggattgtaca aataaatgtg ttgtagatga 950

<210> 163
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 301, 317, 331, 458, 464, 470
<223> n = A,T,C or G

<400> 163
tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagttgt 60
tctccggctg cccattgctc tccactcca cggcgatgtc gctgggatag aagcctttga 120
ccaggcaggt caggctgacc tggttcttgg tcatctcttc ccgggatggg ggcagggtgt 180
acacctgtgg ttctcggggc tgccctttgg ctttgagat ggttttctcg atgggggctg 240
ggaggggcttt gttggagacc ttgcaactgt actccttgc attcaaccag tccctggtgca 300
ngacggtgag gacgctnacc acacggtacg ngctggtgta ctgctcctcc cgcggctttg 360
tcttggcatt atgcacctcc acgccgtcca cgtaccaatt gaacttgacc tcagggtctt 420
cgtggctcac gtccaccacc acgcatgtaa cctcaaanct cggncgcgan cacgc 475

<210> 164
<211> 476
<212> DNA
<213> Homo sapiens

<400> 164
agcgtggctg cggccgaggt ctgaggttac atgcgtgggtg gtggacgtga gccacgaaga 60
ccctgagggtc aagtccaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc agcgtcctca ccgtcctgca 180
ccaggactgg ctgaatggca aggagtacaa gtgcaaggct tccaacaaag ccctcccagc 240
ccccatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac 300
cctgccccca tcccgggagg agatgaccaa gaaccaggct agcctgacct gcctgggtcaa 360
aggcttctat cccagcgaca tcgcccgtgg agtgggagag caatgggcag ccggagaaca 420
actacaagac cacgcctccc gtgctggact ccgacacctg ccgggcggcc gctcga 476

<210> 165

<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 10, 37, 249
<223> n = A,T,C or G

<400> 165
agcgtggttn cggccgaggt cccaaccaag gctgcancct ggatgccatc aaagtcttct 60
gcaacatgga gactggtgag acctgcgtgt accccactca gcccagtgtg gcccagaaga 120
actggtacat cagcaagaac cccaaggaca agaggcatgt ctgggttcggc gagagcatga 180
ccgatggatt ccagttcgag tatggcggcc agggctccga ccctgccgat gtggacctgc 240
ccgggcggnc gctcga 256

<210> 166
<211> 332
<212> DNA
<213> Homo sapiens

<400> 166
agcgtgggtcg cggccgaggt caagaacccc gccgcacct gccgtgacct caagatgtgc 60
cactctgact ggaagagtgg agagtactgg attgaccca accaaggctg caacctggat 120
gccatcaaag tcttctgcaa catggagact ggtgagacct gcgtgtacct cactcagccc 180
agtgtggccc agaagaactg gtacatcagc aagaaccca aggacaagag gcatgtcttg 240
ttcggcgaga gcatgaccga tggattccag ttcgagtatg gcggccaggg ctccgacct 300
gccgatgtgg acctgcccg gcggccgctc ga 332

<210> 167
<211> 332
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 77, 109, 136, 184, 198
<223> n = A,T,C or G

<400> 167
tcgagcggtc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggnat gctctgcgag aaccagacat gcctcttgnc cttgggggttc 120
ttgctgatgt accagntctt ctggggccaca ctgggctgag tggggtacac gcagggtctca 180
ccantctcca tggtgcanaa gactttgatg gcatccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagacagag tggcacatct tgagggtcac gcagggtgcg 300
gcgggggttct tgacctcggt cgcgaccacg ct 332

<210> 168
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 72, 84
<223> n = A,T,C or G

<400> 168

```

tcgagcggcc gcccgggcag gtcctcctca gagcggtagc tggtcttatt gccccggcag 60
cctccataga tnaagttatt gcangagttc ctctccacgt caaagtacca gcgtgggaag 120
gatgcacggc aaggcccagt gactgcgttg gcggtgcagt attcttcata gttgaacata 180
tcgctggagt ggacttcaga atcctgcctt ctgggagcac ttgggacaga ggaatccgct 240
gcattcctgc tgggtggacct cggccgcgac cacgct 276

```

<210> 169

<211> 276

<212> DNA

<213> Homo sapiens

<400> 169

```

agcgtggctc cggccgaggt ccaccagcag gaatgcagcg gattcctctg tcccaggtgc 60
tcccagaagg caggattctg aagaccactc cagcgatatg ttcaactatg aagaatactg 120
caccgccaac gcagtcactg ggccttgccg tgcctccttc ccacgctggt actttgacgt 180
ggagaggaac tcctgcaata acttcatcta tggaggctgc cggggcaata agaacagcta 240
ccgctctgag gaggacctgc ccgggcggcc gctcga 276

```

<210> 170

<211> 332

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 294

<223> n = A,T,C or G

<400> 170

```

tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgt accagttctt ctggggccaca ctgggctgag tgggggtacac gcagggtctca 180
ccagtctcca tggtgcagaa gactttgatg gcatccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagccagaa tggcacatct tgaggtcacg gcangtgccg 300
gcgggggttct tgacctcgcc cgcgaccacg ct 332

```

<210> 171

<211> 333

<212> DNA

<213> Homo sapiens

<400> 171

```

agcgtggctc cggccgaggt caagaaaccc cgcccgacc tgccgtgacc tcaagatgtg 60
ccactctggc tggaagagtg gagagtactg gattgacccc aaccaaggct gcaacctgga 120
tgccatcaaa gtcttctgca acatggagac tgggtgagacc tgcgtgtacc ccactcagcc 180
cagtgtggcc cagaagaact ggtacatcag caagaacccc aaggacaaga ggcatgtctg 240
gctcggcgag agcatgaccg atggattcca gttcgagtat ggcggccagg gctccgaccc 300
tgccgatgtg gacctgcccg ggcggccgct cga 333

```

<210> 172

<211> 527

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 46, 125, 140, 148, 220, 229, 291, 388, 456

<223> n = A,T,C or G

```

<400> 172
agcgtgggtcg cgcccgaggt cctgtcagag tggcactggt agaagntcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctgnaatgg ggcccatgan atggttgntc gagagagagc ttcttgtcct acattcggcg 180
ggtatgggtct tggcctatgc cttatggggg tggccggtgn gggcggtgng gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caaactggtg ttgctgacca naagtgccag 300
gaagctgaat accattttcca gtgtcatacc caggggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctgntc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctgtgtc ttttccttcc aatcangggc tcgctcttct gaatattctt 480
cagggcaatg acataaattg tatattcggg tcccgggtcc aggccag 527

```

<210> 173

<211> 635

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 444, 453, 517, 540, 546, 551, 573, 593

<223> n = A,T,C or G

```

<400> 173
tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctgggtatc atggcagccg 60
ccacgtgccca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtcc ctcggtcccg ccctgggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttcaca cccaatctt 300
catggaccag agatcttggg tgttccttcc acagttcaaa agaccccttt cgtcaccac 360
cctgggtatg aacttgaaa tggatttcag ctctctggca ctcttggtca gcaaccag 420
gttgggcaac aaatgatctt tgangaacat ggntttaggc ggaccacacc ggccacaacg 480
ggcaccacca taaggcatag gccaagaaca taccgncga atgtaggaca agaagctctn 540
tctcanacaa ncatctcatg ggccccattc cangacactt ctgagtacat canttcatg 600
catcctgggtg gcactgataa aaacccttac agtta 635

```

<210> 174

<211> 572

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 457, 511, 520, 552, 568

<223> n = A,T,C or G

```

<400> 174
agcgtgggtcg cggcgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atgggtgtct gagagagagc ttcttgtcct acattcggcg 180
ggtatgggtct tggcctatgc cttatggggg tggccggtgt gggcggtgtg gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caaactggtg ttgctgacca gaagtgccag 300
gaagctgaat accattttcca gtgtcatacc caggggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctggtc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctgtgtc tttttccttc caatcanggg ctgctcttct tgattattct 480
tcagggaatg gacataaatt gtatattcgg ntcccgggtn cagccaataa taataaccct 540
ctgtgacacc anggcggggc cgaagganct ct 572

```

<210> 175

<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 247
<223> n = A,T,C or G

<400> 175
agcgtgggtcg cggccgaggt cctcaccaga ggtaccacct acaacatcat agtggaggca 60
ctgaaagacc agcagaggca taagggttcgg gaagagggtg ttaccgtggg caactctgtc 120
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttanganct ttggaagtgg tcatttcaga tgtgattcat ctagatgggtg ccatgacaat 300
ggtgtgaact acaagattgg agagaagtgg gaccgtcagg gagaaaatgg acctgcccgg 360
gcggccgctc ga 372

<210> 176
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 251
<223> n = A,T,C or G

<400> 176
tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcggt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatccg taggttggtt 240
caagccttcg ntgcagagt tgcccacggg aacaacctct tccgaacct tatgcctctg 300
ctggtctttc agtgcctcca ctatgatgtt gtaggtggta cctctgggtga ggacctcggc 360
cgcgaccacg ct 372

<210> 177
<211> 269
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 94, 225
<223> n = A,T,C or G

<400> 177
agcgtggccg cggccgaggt ccattggctg gaacggcatc aacttggaag ccagtgatcg 60
tctcagcctt gggttctccag ctaatgggtga tggnggtctc agtagcatct gtcacacgag 120
cccttcttg tgggctgaca ttctccagag tggtgacaac accctgagct ggtctgcttg 180
tcaaagtgtc ctttaagagca tagacactca cttcatattt ggcnccacc ataagtcctg 240
atacaaccac ggaatgacct gtcaggaac 269

<210> 178
<211> 529
<212> DNA
<213> Homo sapiens

```

<400> 178
tcgagcggcc gcccgggcag gtcctcagac cgggttctga gtacacagtc agtggtggtg 60
ccttgccagc tgatatggag agccagcccc tgattggaac ccagtccaca gctattcctg 120
caccaactga cctgaagttc actcaggtca caccacaag cctgagcgcc cagtggacac 180
cacccaatgt tcagctcact ggatatcgag tcggttgtag cccaaggag aagaccggac 240
caatgaaaga aatcaacctt gtcctgaca gctcatcgt ggttgatca ggacttatgg 300
cgccaccaaa atatgaagtg agtgtctatg ctcttaagga cactttgaca agcagaccag 360
ctcaggggtg tgtcaccact ctggagaatg tcagcccacc aagaagggt cgtgtgacag 420
atgctactga gaccaccatc accattagct ggagaaccaa gactgagacg atcactggct 480
tccaagttga tgccgttcca gccaatggac ctgcggcgcg accacgctt 529

```

```

<210> 179
<211> 454
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 64
<223> n = A,T,C or G

```

```

<400> 179
agcgtggtcg cgcccgaggt ctggccgaac tgccagtgtg cagggaagat gtacatgtta 60
tagntcttct cgaagtcccg ggccagcagc tccacggggt ggtctcctgc ctccaggcgc 120
ttctcattct catggatctt cttcaccgc agcttctgct tctcagtcag aagggtgttg 180
tctcatccc tctcatcacg ggtgaccagg acgttcttga gccagtcctg catgcgcagg 240
gggaattcgg tcagctcaga gtccaggcaa ggggggatgt atttgcaagg cccgatgtag 300
tccaagtgga gcttgtggcc cttcttggtg ccctccaagg tgcactttgt ggcaaagaag 360
tggcaggaag agtcgaaggt cttgttgtca ttgtgcaca cttctcaaa ctgcaccaatg 420
ggggctgggc agacctgccc gggcggccgc tcga 454

```

```

<210> 180
<211> 454
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 55, 299, 317, 332, 342, 348
<223> n = A,T,C or G

```

```

<400> 180
tcgagcggcc gcccgggcag gtctgcccag ccccatcttg cgagtttgag aaggngtgca 60
gcaatgacaa caagaccttc gactcttcct gccacttctt tgccacaaag tgcaccctgg 120
agggcaccaa gaagggccac aagctccacc tggactacat cgggccttgc aaatacatcc 180
ccccttgccg ggactctgag ctgaccgaat tccccctgcg catgcgggac tggctcaaga 240
acgtcctggt caccctgtat gagagggatg aggacaacaa ccttctgact gagaagcana 300
agctgcgggt gaagaanac catgagaatg anaagcgctt gnaggcanga gaccaccccg 360
tggagctgct ggcccgggac ttcgagaaga actataacat gtacatcttc cctgtacact 420
ggcagttcgg ccagacctcg gccgcgacca cgct 454

```

```

<210> 181
<211> 102
<212> DNA
<213> Homo sapiens

```

```

<220>

```

<221> misc_feature
 <222> 8, 47, 60, 67
 <223> n = A,T,C or G

<400> 181
 agcgtggntg cggacgacgc ccacaaagcc attgtatgta gttttanttc agctgcaaan 60
 aataccncca gcatccacct tactaaccag catatgcaga ca 102

<210> 182
 <211> 337
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 169, 195, 253, 314
 <223> n = A,T,C or G

<400> 182
 tcgagcggtc gcccgggcag gtctgggcgg atagcaccgg gcatattttg gaatggatga 60
 ggtctggcac cctgagcagc ccagcgagga cttggtctta gttgagcaat ttggctagga 120
 ggatagtatg cagcacgggt ctgagtctgt gggatagctg ccatgaagna acctgaagga 180
 ggcgctggct ggtanggggt gattacaggg ctgggaacag ctggtacact tgccattctc 240
 tgcataact ggntagttag gcgagcctgg cgctcttctt tgcgctgagc taaagctaca 300
 tacaatggct ttgnggacct cgccgcgcac cagcgtt 337

<210> 183
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 183
 tcgagcgggc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60
 gtagttcaca ccattgtcat gacaccatct agatgaatca catctgaaat gaccacttcc 120
 aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
 tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcattcg taggttggtt 240
 caagccttcg ttgacagaag ttgccacagg taacaacctc tccccgaacc ttatgcctct 300
 gctggctctt caagtgcctc cactatgatg ttgtagggtg caoctctggt gaggacctcg 360
 gccgcgacca cgct 374

<210> 184
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 30, 174, 248, 285, 306, 332, 345, 368
 <223> n = A,T,C or G

<400> 184
 agcgtggttt gcggccgagg tcctcaccan aggtgccacc tacaacatca tagtggaggc 60
 actgaaagac cagcagaggc ataagggttcg ggaagagggt gttaccgtgg gcaactctgt 120
 caacgaaggc ttgaaccaac ctacggatga ctgctgcttt gaccctaca cagnttccca 180
 ttatgccgtt ggagatgagt gggaacgaat gtctgaatca ggcttttaac tgttggtgcca 240
 gtgcttangc tttggaagtg gtcatttcag atgtgattca tctanatggt gtcattgaca 300
 tgggtngaac tacaagattg gagagaagtg gnaccgtcag ggganaaaat ggacctgccc 360
 ggccggcncg ctcga 375

<210> 185
 <211> 148
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 28, 36, 86
 <223> n = A,T,C or G

<400> 185
 agcgtgggtcg cgcccgaggt ctggcttct gctcangtga ttatcctgaa ccatccaggc 60
 caaataagcg ccggctatgc ccctgnattg gattgccaca cggtcacat tgcattgcaag 120
 tttgctgagc tgaaggaaaa gattgac 148

<210> 186
 <211> 397
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 78
 <223> n = A,T,C or G

<400> 186
 tcgagcggcc gcccgggcag gtccaattga aacaaacagt tctgagaccg ttcttccacc 60
 actgattaag agtgggngg cggtattag ggataatatt catttagcct tctgagcttt 120
 ctgggcagac ttggtgacct tgccagctcc agcagccttc tgggtccactg ctttgatgac 180
 acccaccgca actgtctgtc tcatatcacg aacagcaaag cgacccaaag gtggatagtc 240
 tgagaagctc tcaacacaca tgggcttgcc aggaaccata tcaacaatgg gcagcatcac 300
 cagacttcaa gaatttaagg gccatcttcc agctttttac cagaacggcg atcaatcttt 360
 tccttcagct cagcaaactt gcatgcaatg tgagccg 397

<210> 187
 <211> 584
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 145, 286, 363, 365, 425, 433, 452, 462, 471, 512, 514, 534,
 536, 540, 565, 583
 <223> n = A,T,C or G

<400> 187
 tcgagcggcc gcccgggcag gtccagaggg ctgtgctgaa gtttgctgct gccactggag 60
 ccactccaat tgctggccgc ttactcctg gaaccttcac taaccagatc caggcagcct 120
 tccgggagcc acggcttctt gtggntactg accccagggc tgaccaccag cctctcacgg 180
 aggcatttta tgtaacctt cctaccattg cgctgtgtaa cacagattct cctctgogct 240
 atgtggacat tgccatccca tgcaacaaca agggagctca ctgagngggg tttgatgtgg 300
 tggatgctgg ctcggaagt tctgcgcatg cgtggcacca tttcccgtga acacccatgg 360
 gangncatgc ctgatctgga cttctacaga gatcctgaag agattgaaaa agaagaacag 420
 gctgnttgct ganaaagcaa gtgaccaagg angaaatttc anggggtgaaa nggactgctc 480
 ccgctcctga attcactgct actcaacctg angntgcaga ctgggtcttga aggnagnacan 540
 gggccctctg ggccatttta agcancttcg gtcgcgaaca cgnt 584

<210> 188
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 7, 136, 486
<223> n = A,T,C or G

<400> 188
agcgtgngtc gcggccgagg tgctgaatag gcacagaggg cacctgtaca ccttcagacc 60
agtctgcaac ctcaggctga gtagcagtga actcaggagc gggagcagtc cattcaccct 120
gaaattcctc cttggncaact gccttctcag cagcagcctg ctcttctttt tcaatctctt 180
caggatctct gtagaagtac agatcaggca tgacctcca tgggtgttca cgggaaatgg 240
tgccacgcat gcgcagaact tcccagacca gcattccacca catcaaacc actgagttag 300
ctcccttggt gttgcatggg atgggcaatg tccacatagc gcagaggaga atctgtgtta 360
cacagcgcaa tggtaggtag gttaacataa gatgcctccg cgagaagctg gtggtcagcc 420
ctgggggtcaa gtaaccacaa gaagccgtgg ctcccgggaag gctgcctgga tctggttagt 480
gaaggntcca ggagtgaagc ggccaacaat tggagtgggt tcagtggcaa gcagcaaact 540
tcagcacaag ccctctggac ctgcccggcg gccgctcga 579

<210> 189
<211> 374
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 41, 280, 314, 330, 350, 353
<223> n = A,T,C or G

<400> 189
tcgagcgggc gcccgggcag gtccattttc tccctgacgg nccacttct ctccaatctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatccg taggttggtt 240
caagccttcg ttgacagagt tgccacgggt aacaacctcn tcccgaacc ttatgcctct 300
gctgggcttt cagngcctcc actatgatgn tgtagggggg cacctctggn gangacctcg 360
gccgcgacca cgct 374

<210> 190
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 247, 304, 306, 332, 337
<223> n = A,T,C or G

<400> 190
agcgtggctc cggccgaggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60
ctgaaagacc agcagaggca taaggctcgg gaagagggtt ttaccgtggg caactctgtc 120
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttccat 180
tatgccgttg gagatgagt ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttangct ttggaagtgg gtcatctcag atgtgattca tctagatggt gccatgacaa 300
tggngngaac tacaagattg gagagaagtg gnaccgncag ggagaaaatg gacctgccc 360

ggcggccgct cga

373

<210> 191

<211> 354

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 218, 299, 306, 326, 333, 337, 341

<223> n = A,T,C or G

<400> 191

```

agcgtgggtcg cggccgaggt ccacatcggc aggggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggntg caaccttggg tgggggtcaat 240
ccagtactct ccactcttcc agccagagtg gcacatcttg aggtcacggc aggtgcggnc 300
gggggntttt gcggtgccc tctggncttc ggntgtntct natctgctgg ctca 354

```

<210> 192

<211> 587

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 276

<223> n = A,T,C or G

<400> 192

```

tcgagcggcc gcccgggcag gtctcgcggt cgcactgggt atgctgggtcc tgttggtccc 60
cccggccctc ctggacctcc tggccccctt ggtcctccca gcgtgggtt cgacttcagc 120
ttcctgcccc agccacctca agagaaggct cacgatgggt gccgtacta ccgggctgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagcctgagc 240
cagcagatcg agaacatccg gagcccagag ggcagncgca agaaccctgc ccgcacctgc 300
cgtgacctca agatgtgcc aactgactgg aagagtggag agtactggat tgaccccaac 360
caagctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggg gagacctgcg 420
tgtaccccac tcagcccagt gtggcccaaa agaactggta catcagcaag aaccccaagg 480
acaagaagca tgtctgggtc ggcgagaaca tgaccgatgg attccagttc gagtatggcg 540
ggcagggctc cgaccctgcc gatggggacc ttggccgcga acacgct 587

```

<210> 193

<211> 98

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 9, 33, 58, 71, 90

<223> n = A,T,C or G

<400> 193

```

agcgtggng cggccgaggt ataaatatcc agnccatctc ctccctccac acgctganag 60
atgaagctgt ncaaagatct cagggtggan aaaacct 98

```

<210> 194

<211> 240

<212> DNA

<213> Homo sapiens

<400> 194

```

tcgagcggcc gcccgggcag gtccttcaga cttggactgt gtcacactgc caggcttcca 60
gggctccaac ttgcagacgg cctgttggtg gacagtctct gtaatcgcg aagcaacccat 120
ggaagacctg ggggaaaaca ccatggtttt atccaccctg agatctttga acaacttcat 180
ctctcagcgt gcggaggag gctctggact ggatatttct acctcggccg cgaccacgct 240

```

<210> 195

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 22, 37, 39, 105, 268, 276, 302, 323, 331, 335, 347, 351, 371, 378

<223> n = A,T,C or G

<400> 195

```

cgagcgggcg accgggcagg tncagactcc aatccanana accatcaagc cagatgtcag 60
aagctacacc atcacagggt tacaaccagg cactgactac aaganctacc tgcacacctt 120
gaatgacaat gctcggagct cccctgtggt catcgacgcc tccactgcc a ttgatgcacc 180
atccaacctg cgtttccttg ccaccacacc caattccttg ctggtatcat ggcagccgcc 240
acgtgccagg attaccggt a catcatcnag tatganaagc ctgggcctcc tcccagagaa 300
gnggtccctc ggccccgcc tgntgtccca naggntacta ttactgngcc ngcaaccggc 360
aaccgatatc nattttgnca ttggccttca acaataatta 400

```

<210> 196

<211> 494

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 19, 83, 168, 252, 271, 292, 430

<223> n = A,T,C or G

<400> 196

```

agcgtggttc gcggccgang tcctgtcaga gtggcactgg tagaagttcc aggaaccctg 60
aactgtaagg gttcttcatac agngccaaca ggatgacatg aaatgatgta ctcagaagtg 120
tcctggaatg gggcccatga gatggttgtc tgagagagag cttcttgnc tgtctttttc 180
cttccaatca ggggctcgct cttctgatta ttcttcaggg caatgacata aattgtatat 240
tcgggtcccg gntccaggcc agtaatagta ncctctgtga caccagggcg gngccgaggg 300
accacttctc tgggaggaga cccaggcttc tcatacttga tgatgtaacc ggtaatcctg 360
gcacgtggcg gctgccatga taccagcaag gaattgggggt gtggtggcca ggaaacgcag 420
gttgatgggn gcatcaatgg cagtggaggc cgtcgatgac cacaggggga gctccgacat 480
tgtcattcaa ggtg

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<210> 197

<211> 118

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 71, 96

<223> n = A,T,C or G

<400> 197

agcgtggncg cggccgaggt gcagcgcggg ctgtgccacc ttctgctctc tgcccaacga 60
taaggagggt ncctgcccc aggagaacat taactntccc cagctcggcc tctgccgg 118

<210> 198

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 41, 53, 98, 195, 350

<223> n = A,T,C or G

<400> 198

tgcagcggcc gcccgggcag gttttttttg ctgaaagtgg ntactttatt ggntgggaaa 60
gggagaagct gtggtcagcc caagagggaa tacagagncc cgaaaaaggg gagggcaggt 120
gggctggaac cagacgcagg gccaggcaga aactttctct cctcactgct cagcctgggtg 180
gtggctggag ctcanaaatt gggagtgcac caggacacct tcccacagcc attgcggcgg 240
catttcattt ggccaggaca ctggctgtcc acctggcact ggtcccagca gaagcccag 300
ctggggaaag ttaatgttca cctgggggca ggaacctcc ttatcattgn gcagagagca 360
gaaggtggca cagcccgcgc tgcacctcgg ccgcgaccac gct 403

<210> 199

<211> 167

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 92, 107

<223> n = A,T,C or G

<400> 199

tgcagcggcc gcccgggcag gtccaccata agtcctgata caaccacgga tgagctgtca 60
ggagcaaggt tgattttctt cattgggtccg gnccttctct tgggggncac ccgcactcga 120
tatccagtga gctgaacatt ggggtggcgc cactgggcgc tcaggct 167

<210> 200

<211> 252

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 210, 226, 227, 230, 236

<223> n = A,T,C or G

<400> 200

tgcagcgggt cggccgggca ggtccaccac acccaattcc ttgctgggtat catggcagcc 60
gccacgtgcc aggattaccg gctacatcat caagtatgag aagcctgggt ctctcccag 120
agaagcggtc cctcggcccc gccctgggtg cacagaggct actattactg gcctggaacc 180
gggaaccgaa tatacaattt atgtcattgn cctgaagaat aatcannaan agcgancccc 240
tgattggaag ga 252

<210> 201
 <211> 91
 <212> DNA
 <213> Homo sapiens

<400> 201
 agcgtggtcg cgcccgaggt tgtacaagct tttttttttt tttttttttt tttttttttt 60
 tttttttttt tttttttttt tttttttttt t 91

<210> 202
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 9, 354
 <223> n = A,T,C or G

<400> 202
 tcgagcggnc gcccgggcag gtctgccaac accaagattg gcccccgccg catccacaca 60
 gtccgtgtgc ggggaggtaa caagaaatac cgtgccctga gggtggacgt gggaatttc 120
 tcctggggct cagagtgttg tactcgtaaa acaaggatca tcgatgttgt ctacaatgca 180
 tctaataacg agctggttcg taccaagacc ctggtgaaga attgcatcgt gctcatcgac 240
 agcacaccgt accgacagtg gtacgagtc cactatgcgc tgccccctgg ccgcaagaag 300
 ggagccaagc tgactcctga ggaagaagag attttaaaca aaaaacgac taanaaaaaa 360
 aaaacaat 368

<210> 203
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 203
 agcgtggtcg cgcccgaggt gaaatggtat tcagcttcct ggcaattctg gtcagcaacc 60
 cagtgttggg caacaaatga tctttgagga acatggtttt aggcggacca caccgcccac 120
 aacggccacc ccataaggc ataggccaag accatacccg ccgaatgtag gacaagaagc 180
 tctctctcag acaaccatct catgggcccc attccaggac acttctgagt acatcatttc 240
 atgtcatcct gttggcactg atgaagaacc cttacagttc agggttcctg gaactttctac 300
 cagtgcact ctgacaggac ctgcccgggc ggccgctcga 340

<210> 204
 <211> 341
 <212> DNA
 <213> Homo sapiens

<400> 204
 tcgagcggcc gcccgggcag gtccgtgcag agtggcactg gtagaagttc caggaaccct 60
 gaactgtaag ggttcttcat cagtgccaac aggatgacat gaaatgatgt actcagaagt 120
 gtcctggaat gggggccatg agatggttgt ctgagagaga gcttcttctg ctacattcgg 180
 cgggtatggt cttggcctat gccttatggg ggtggccggt gtgggcggtg tgggccgcct 240
 aaaaccatgt tcctcaaaga tcatttggtt cccaacactg ggttgctgac cagaagtgcc 300
 aggaagctga ataccatttc acctcggccg cgaccacgct a 341

<210> 205
 <211> 770
 <212> DNA
 <213> Homo sapiens

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<220>
<221> misc_feature
<222> 529, 591, 623, 626, 629, 630, 656, 702, 709, 712, 717, 743,
746, 749, 759, 762, 766
<223> n = A,T,C or G

<400> 205
tcgagcggcc gcccgggcag gtctcccttc ttgcgggcca ggggcagcgc atagtgggac 60
tcgtaccact gtcggtacgg tgtgctgtcg atgagcacga tgcaattctt caccagggtc 120
ttggtacgaa ccagctcggt attagatgca ttgtagacaa catcgatgat ccttggttta 180
cgagtacaac actctgagcc ccaggagaaa ttccccacgt ccaacctcag ggcacgggat 240
ttcttggtac ctccccgcac acggactgtg tggatgcggc gggggccaag ctgactcctg 300
aggaagaaga gatttttaac aaaaaacgat ctaaaaaaat tcagaagaaa tatgatgaaa 360
ggaaaaagaa tgccaaaatc agcagtctcc tggaggagca gttccagcag ggcaagcttc 420
ttgcgtgcat cgcttcaagg ccgggacagt gtgaccgagc agatggctat gtgctagagg 480
gcaaagaagt ggagttctat ctttaagaaaa tcaggggcca gaatgggtng tcttcaacta 540
atccaaaggg gagtttcaga ccagtgcagt cagcaaaaac attgatactg ntggccaaat 600
ttattggtgc agggcttgca cantangann ggctgggtct tggggcttgg attggnacaa 660
gctttggcag ccttttcttt ggttttgcca aaaacctttt gntgaagang anacctnggg 720
cggaccctt aaccgattcc acnccngng gcgttctang gncccncttg 770

<210> 206
<211> 810
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 574, 621, 625, 636, 668, 673, 704, 728, 743, 767, 772, 786,
789, 807, 809, 810
<223> n = A,T,C or G

<400> 206
agcgtggctc cgcccgaggt ctgctgcttc agcgaagggt ttctggcata accaatgata 60
aggetgccaa agactgttcc aataccagca ccagaaccag ccactcctac tgttgagca 120
cctgcaccaa taaatttggc agcagtatca atgtctctgc tgattgcact ggtctgaaac 180
tccctttgga ttagctgaga cacaccattc tggggcctga ttttcctaag atagaactcc 240
aactctttgc cctctagcac atagccatct gctcggtcac actgtcccgg ccttgaagcg 300
atgcacgcaa gaagcttgcc ctgctggaac tgctcctcca ggagactgct gattttggca 360
ttctttttcc tttcatcata tttcttctga atttttttag atcgtttttt gtttaaaatc 420
tcttcttcct caggagtcag cttggccccc gcgcaccca cacagtccgt gtgcggggag 480
gtaacaagaa ataccgtgcc ctgaggttgg acgtggggaa tttctcctgg ggctcagagt 540
gggtgtactc taaaacaagg atcatcgatg gtgnctacaa tgcactaat aacgagctgg 600
gtcggaccca aagaacctgg ngaanaaatg gatognctca tcgacaggac accgtaccgg 660
acaggggnac gantccact atgcgcttgc ccctgggccg caanaaagga aaactgcccg 720
ggcggccntc gaaagcccaa ttntggaaaa aatccatcac actgggnggc cngtcgagca 780
tgcattntana ggggcccatt cccctnnann

<210> 207
<211> 257
<212> DNA
<213> Homo sapiens

<400> 207
tcgagcggcc gcccgggcag gtccccaacc aaggctgcaa cctggatgcc atcaaagtct 60
tctgcaacat ggagactggg gagacctgcg tgtacccac tcagcccagt gtggcccaga 120
agaactggta catcagcaag aaccccaagg acaagaggca tgtctggttc ggcgagagca 180

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tgaccgatgg attccagttc gagtatggcg gccagggctc cgaccctgcc gatgtggacc 240
tcggccgcga ccacgct 257

<210> 208

<211> 257

<212> DNA

<213> Homo sapiens

<400> 208

agcgtgggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccagggtg cagccttggg tggggacctg 240
cccgggcggc cgctcga 257

<210> 209

<211> 747

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 453, 538, 540, 542, 546, 554, 556, 598, 659, 670, 679, 689,
693, 711, 723, 724, 731, 747

<223> n = A,T,C or G

<400> 209

tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctgggtatc atggcagccg 60
ccacgtgccg ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtcc ctcgccccc cctgggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttcaca cccaatctt 300
catggaccag agatcttgga tgttccttcc acagttcaaa agaccctttt cgtcaccac 360
cctgggtatg acactggaaa tgggtattcag cttoctggca cttctgggtc gcaaccag 420
gttgggcaac aaatgatctt tgaggaacat ggntttaggc ggaccacacc gccacaacg 480
gccaccccc taaggcatag gccaagacca taccgcccga atgtaggaca agaagctntn 540
tntcanacac catntnatgg gcccattcc aggacacttc tgagtacatc atttatgnca 600
tctgtggcac ttgatgaaaa cccttacagt tcagggttct ggaactttta ccaggcctnt 660
tacaggactn ggccggacnc cttaagcna ttncaccctg gggcggttcta nggtcccact 720
cgnnactgg ngaaaatggc tactgtn 747

<210> 210

<211> 872

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 165, 174, 181, 256, 260, 269, 271, 277, 286, 289, 294, 298,
300, 301, 303, 308, 311, 321, 325, 328, 329, 333, 338, 342,
346, 349, 351, 357, 359, 364, 366, 379, 385, 395, 396, 397,
407, 408, 410, 414, 415, 429, 431, 434, 435, 440, 443

<223> n = A,T,C or G

<221> misc_feature

<222> 444, 446, 447, 448, 449, 450, 451, 464, 470, 472, 475, 479,
483, 484, 485, 488, 494, 496, 497, 504, 508, 509, 511, 513,
517, 522, 524, 526, 532, 533, 542, 543, 553, 559, 566, 567,

571, 572, 578, 582, 588, 591, 594, 595, 596, 600, 606

<223> n = A,T,C or G

<221> misc_feature

<222> 612, 614, 617, 618, 629, 630, 631, 652, 654, 655, 661, 663,
664, 666, 671, 673, 678, 679, 681, 688, 690, 691, 698, 706,
707, 708, 714, 719, 721, 723, 726, 741, 751, 761, 762, 769,
770, 778, 779, 781, 782, 785, 791, 802, 807, 808, 812

<223> n = A,T,C or G

<221> misc_feature

<222> 815, 820, 827, 828, 838, 841, 844, 851, 857, 864, 866, 869,
872

<223> n = A,T,C or G

<400> 210

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agcgtggtcg cgcccgaggt ccactagagg tctgtgtgcc attgcccagg cagagtctct 60
gcgttacaaa ctcctaggag ggcttgcgtg gcggagggcc tgctatggtg tgctgcggtt 120
catcatggag agtggggcca aaggctgcga ggtgtggtg tctgngaaac tccnaggaca 180
ngagggctaa attccatgaa gtttgtggat ggctgatga tccacaatcg gagaccctgt 240
taactactac cgtctnaccn cctgctgtnc nccccnttt ctgctnaana catngggntn 300
ntncttgnc ntccttgggt ngaanatnna atngcctncc cnttctanc nctactngnt 360
ccananttgg cctttaaana atccncttg cctnnnnac tgttcanntn tttntctgta 420
aacctatna nttnnattan atnntnnnn nctcaccccc ctctcattn anccnatang 480
ctnnnaantc cttannnct cccnccnnt ncnctentac tnantncttc tnnccatta 540
cnnagctctt tcntttaana taatgnngcc nngctctnca tntctacnat ntgnnaatn 600
ccccncccc cnancgnntt tttgacctnn naacctcctt tcctcttccc tncnnaaatt 660
ncnnanttcc ncnttcnnc ntttcggntn ntccatnct ttcannnct tcantctanc 720
ncnctncaac ttattttcct ntcacccctt nttctttaca nccccctnn tctactcnc 780
nnttncatta natttgaaac tnccacnct antnccctn ctctacnntt ttattttncg 840
ntcnctctac ntaatanntt aatnantnt cn 872

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<210> 211

<211> 517

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 462, 464, 506

<223> n = A,T,C or G

<400> 211

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tcgagcggcc gcccgggcag gtctgccaag gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggctctg gcttcccacc cttctgttct gagatggggg tgggtggcag 120
tatctcatct ttgggttcca caatgctcac gtggtcaggc aggggcttct tagggccaat 180
cttaccagtt ggggtcccagg gcagcatgat cttcaccttg atgcccagca caccctgtct 240
gagcaacacg tggcgcaaaa gcagtgtcaa cgtagtaagt taacagggtc tccgctgtgg 300
atcatcaggc catccacaaa cttcatggat ttagccctct gtccctggag tttcccagac 360
accacaacct cgcagccttt ggccccactc tccatgatga accgcagcac accatagcag 420
gccctccgca caagcaagcc ctctaagaa tttgtaacgc ananactctg ctggcaatgg 480
cacacaaacc tctagtggac ctcgngcgcg accacgc 517

```

<210> 212

<211> 695

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> 432, 476, 522, 547, 621, 624, 647, 679
 <223> n = A,T,C or G

<400> 212
 tcgagcggcc gcccgggcag gtctgggtcca ggatagcctg cgagtcctcc tactgctact 60
 ccagacttga catcatatga atcatactgg ggagaatagt tctgaggacc agtagggcat 120
 gattcacaga ttccaggggg gccaggagaa ccaggggacc ctgggtgtcc tggaatacca 180
 ggggtcaccat ttctcccagg aataccagga gggcctggat ctcccttggg gccttgaggt 240
 ccttgaccat taggagggcg agtaggagca gttggaggct gtgggcaaac tgcacaaat 300
 tctccaaatg gaatttctgg gttggggcag tctaattctt gatccgtcac atattatgtc 360
 atcgcacaga acggatcctg agtcacagac acatatttgg catggttctg gcttccagac 420
 atctctatcc gncataggac tgaccaagat gggaacatcc tccttcaaca agcttnctgt 480
 tgtgcaaaaa ataatagtgg gatgaagcag accgagaagt anccagctcc cctttttgca 540
 caaagcntca tcatgtctaa atatcagaca tgagacttct ttggggcaaaa aaggagaaaa 600
 agaaaaagca gttcaaagta nccnccatca agttgggttc ttgcccnttc agcaccggg 660
 ccccggttata aaacacctng ggccgggacc ccctt 695

<210> 213
 <211> 804
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 552, 555, 592, 624, 629, 633, 658, 695, 697, 698, 700, 702,
 745, 753, 755, 762, 773, 786, 788, 793, 795
 <223> n = A,T,C or G

<400> 213
 agcgtggctg cggccgaggt gttttatgac gggcccgggtg ctgaagggca gggaacaact 60
 tgatgggtgct actttgaact gcttttcttt tctccttttt gcacaaagag tctcatgtct 120
 gatattttaga catgatgagc tttgtgcaaa aggggagctg gctacttctc gctctgcttc 180
 atcccactat tattttggca caacaggaag ctggtgaagg aggatgttcc catcttgggtc 240
 agtcctatgc ggatagagat gtctggaagc cagaaccatg ccaaatatgt gtctgtgact 300
 caggatccgt tctctgcatgac gacataatat gtgacgatca agaattagac tgccccaacc 360
 cagaaattcc atttggagaa tgttgtgcag tttgccaca gcctccaact gctcctactc 420
 gccctcctaa tgggtcaagga cctcaaggcc ccaagggaga tccaggccct cctgggtattc 480
 ctggggagaaa tgggtgaccct ggtattccag gacaaccagg gtcccttgggt tctcctggcc 540
 cccttggat cngngaatc atgcccact ggtcctcaaa ctattctccc anatgattca 600
 tatgatgtca agtctgggat agcnagtang ganggactcg caggctattc tggaccanac 660
 ctgccggggg ggcgttcgaa agcccgaatc tgcananntn cnttcacact ggcggccgctc 720
 gagctgcttt aaaagggcc ttcnccttt agnngngggg antacaatta ctngggcgcg 780
 ttttanancg cngnctggg aaat 804

<210> 214
 <211> 594
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 452, 509, 585
 <223> n = A,T,C or G

<400> 214
 agcgtggctg cggccgaggt ccacatcggc agggctggag ccctggccgc catactcgaa 60

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ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgtcct tgggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccagggtg cagccttggg tgggggtcaat 240
ccagtactct ccaactcttcc agtcagagtg gcacatcttg aggtcacggc aggtgcgggc 300
gggggttcttg cggctgccct ctgggctccg gatgttctcg atctgctggc tcagggtctt 360
gaggggtggtg tccacctcga ggtcacggtc acgaaccaca ttggcatcat cagcccggta 420
gtagcggcca ccatcgtag ccttctcttg angtggctgg ggcaggaact gaagtcgaaa 480
ccagcgctgg gaggaccagg gggaccaana ggtccaggaa gggcccgggg gggaccaaca 540
ggaccagcat caccaagtgc gacccgcgag aacctgcccg gccgnccgct cgaa 594

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<210> 215

<211> 590

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 9

<223> n = A,T,C or G

<400> 215

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cccggccctc ctggacctcc tggccccct ggtcctccca gcgctgggtt cgacttcagc 120
ttcctgcccc agccacctca agagaaggct cacgatgggtg gccgctacta ccgggctgat 180
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cagcagatcg agaacatccg gagcccagag ggcagccgca agaaccgcc cgcacctgc 300
cgtgacctca agatgtgcc aactgactgg aagagtggag agtactggat tgaccccaac 360
caaggctgca acctggatgc catcaaagtc ttctgcaaca tggagactgg tgagacctgc 420
gtgtacccca ctcagcccag tgtggcccag aagaactggg acatcagcaa gaacccaag 480
gacaagaggc atgtctggtt cggcgagagc atgaccgatg gattccagtt cgagtatggc 540
ggccagggtc cccacctgc cgatgtggac ctccggccgc gaccacctt 594

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<210> 216

<211> 801

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 2, 22, 25, 26, 328, 373, 385, 440, 473, 534, 571, 572, 573, 582, 587, 589, 593, 600, 605, 617, 633, 642, 653, 672, 681, 685, 696, 699, 709, 715, 717, 726, 731, 739, 742, 745, 758, 769, 772, 778, 780, 788, 789, 791, 793, 796

<223> n = A,T,C or G

<400> 216

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tngagcggcc gcccgggag gntgnnaacg ctggtcctgc tggctcctct ggcaagggtg 60
gtgaagatgg tcacctgga aaaccggac gacctggtga gagaggagtt gttggaccac 120
aggggtgctcg tggtttccct ggaactcctg gacttcctgg cttcaaaggc attaggggac 180
acaatggtct ggatggattg aagggacagc ccggtgctcc tgggtggaag ggtgaacctg 240
gtgcccctgg tgaaaatgga actccaggtc aaacaggagc ccgtgggctt cctgggtgaga 300
gaggaccgtg ttggtgcccc tggcccanac ctccggccgc accacgctaa gccgaattt 360
ccagcacact ggnggccgtt actantggat ccgagctcgg taccaagctt ggcgtaatca 420
tggatcatagc tgtttctctg gtgaaattgt tatccgctca caatttcaca cancatacga 480
agccggaaaag cataaagtgt aaagccttgg ggtgctaata agtgagctaa ctncattaa 540
attgcggttg gctcactgcc cgcttttcca nnnnggaaac cntggcntng ccngcttgc 600
ttaantgaaa tccgccnacc cccggggaaa agncgggttg cngtattggg gcnccttttc 660
cctttcctcg gnttacttga nttantgggc ttggnccgnt tcgggttgng gcganccggt 720

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tcaacntcac nccaaaggng gnaanacggt tttcccanaa tccgggggnt ancccaangn 780
 aaaacatnng ncnaangggc t 801

<210> 217
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 10, 157, 170
 <223> n = A,T,C or G

<400> 217
 agcgtggttn gcggccgagg tctgggccag gggcaccaac acgtcctctc tcaccaggaa 60
 gccacgggc tctgtttga cctggagttc cattttcacc aggggcacca ggttcaccct 120
 tcacaccagg agcaccgggc tgtcccttca atccatncag accattgtgn cccctaatac 180
 ctttgaagcc aggaagtcca ggagttccag ggaaaccacc gagcaccctg tggccaaca 240
 actcctctct caccaggctg tccgggtttt ccagggtgac catcttcacc agccttgcca 300
 ggaggaccag caggaccagc gttaccaacc tgcccgggag gccgctcga 349

<210> 218
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 218
 tcgagcgcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60
 gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
 aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
 tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240
 caagccttcg ttgacagagt tgcccacggg aacaacctct tcccgaacct tatgcctctg 300
 ctggtctttc agtgcctcca ctatgatgtt gtaggtggca cctctggtga ggacctcggc 360
 cgcgaccacg ct 372

<210> 219
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 219
 agcgtggtcg cgcccgaggc cctcaccaga ggtgccacct acaacatcat agtggaggca 60
 ctgaaagacc agcagaggca taagggtcgg gaagagggtg ttaccgtggg caactctgtc 120
 aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
 tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
 tgcttaggct ttggaagtgg tcatttcaag atgtgattca tctagatggt gccatgacaa 300
 tgggtgtgaac tacaagattg gagagaagtg ggaccgtcag ggagaaaatg gacctgcccg 360
 ggccggccgc tcga 374

<210> 220
 <211> 828
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 8, 9, 557, 571, 587, 588, 601, 642, 643, 647, 654, 664, 681,
 688, 698, 719, 720, 725, 734, 738, 743, 744, 757, 765, 773,

778, 780, 782, 783, 793, 798, 805, 809, 822, 827

<223> n = A,T,C or G

<400> 220

```

tcgagcggnnc gcccgggcag gtccagtagt gccttcggga ctgggttcac cccaggtct 60
gcggcagttg tcacagcgcc agccccgctg gcctccaaag catgtgcagg agcaaattggc 120
accgagatat tccttctgcc actgttctcc tacgtggtat gtcttcccat catcgtaaca 180
cgttgcctca tgagggtcac acttgaattc tccttttccg ttccaagac atgtgcagct 240
catttggtcg gctctatagt ttggggaaag ttgttgaaa ctgtgccact gacctttact 300
tcctccttct ctactggagc ttctgtacct tccacttctg ctgttggtaa aatgggtgat 360
cttctatcaa ttctattgac agtaccact tctccaaaac atccaggga atagtgtttt 420
cagagcgatt aggagaacca aattatgggg cagaaataag gggttttcc acaggttttc 480
ctttggagga agatttcagt ggtgacttta aaagaatact caacagtgtc ttcattccca 540
tagcaaaaga agaaacngta aatgatggaa ngcttctgga gatgccnnca ttttaaggga 600
ncccagaact tcaccatcta caggacctac ttcagtttac annaagncac atantctgac 660
tcanaaagga ccaagtagc nccatggnc gcactttttag cctttcccct ggggaaaann 720
ttacnttctt aaancctngg ccnngacccc ctttaagncca aattntggaa aanttccntn 780
cnnctggggg gcngttcnac atgcntttta agggcccaat tncacct 828

```

<210> 221

<211> 476

<212> DNA

<213> Homo sapiens

<400> 221

```

tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtgggc ttgtagttgt 60
tctccggctg cccattgctc tccactcca cggcgatgtc gctgggatag aagcctttga 120
ccaggcaggt caggctgacc tggttcttgg tcatctctc ccgggatggg ggagggtgt 180
acacctgtgg ttctcggggc tgcccttgg ctttgagat ggttttctcg atgggggtg 240
ggagggttt gtggagacc ttgacttgt actccttggc attcagccag tctgtgtgca 300
ggacggtgag gacgctgacc acacggtacg tgctgttgta ctgctcctcc cgcggctttg 360
tcttggcatt atgcacctcc acgccgtcca cgtaccagtt gaacttgacc tcagggtctt 420
cgtggctcac gtccaccacc acgcatgtaa cctcagacct cggccgcgac cacgct 476

```

<210> 222

<211> 477

<212> DNA

<213> Homo sapiens

<400> 222

```

agcgtggctg cggccgaggt ctgaggttac atgcgtgggt gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gccgcgggag gagcagtaca acagcacgta ccgtgtgggc agcgtcctca ccgtcctgca 180
ccaggactgg ctgaatggca aggagtacaa gtgcaaggte tccaacaaag ccctccagc 240
ccccatcgag aaaaccatct ccaaagccaa agggcaagcc ccgagaacca caggtgtaca 300
ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc tgctgtgtca 360
aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca 420
actacaagac cagcctccc gtgctggact ccgacacctg cccgggcggc cgctcga 477

```

<210> 223

<211> 361

<212> DNA

<213> Homo sapiens

<400> 223

```

tcgagcggcc gcccgggcag gttgaatggc tctcgtgta ccacccgggt gctgggtgtg 60
ggtacagagc tccgatgggt gaaaccattg acatagagac tgtccctgtc cagggtgtag 120
gggcccagct cagtgatgcc gtgggtcagc tggctcagct tccagtacag ccgtctctg 180

```

```
tccagtccag ggcttttggg gtcaggacga tgggtgcaga cagcatccac tctggtggct 240
gccccatcct tctcaggcct gagcaaggtc agtctgcaac cagagtacag agagctgaca 300
ctggtgttct tgaacaaggg cataagcaga ccctgaagga cacctcggcc gcgaccacgc 360
t 361
```

<210> 224

<211> 361

<212> DNA

<213> Homo sapiens

<400> 224

```
agcgtgggtcg cgcccgaggt gtccttcagg gtctgcttat gcccttggtc aagaacacca 60
gtgtcagctc tctgtactct gggtgcagac tgaccttgct caggcctgag aaggatggg 120
cagccaccag agtggatgct gtctgcaccc atcgtcctga ccccaaaagc cctggactgg 180
acagagagcg gctgtactgg aagctgagcc agctgaccca cggcatact gagctgggcc 240
cctacaccct ggacagggac agtctctatg tcaatggttt caccatcgg agctctgtac 300
ccaccaccag caccgggggtg gtcagcgagg agccattcaa cctgcccggg cggccgctcg 360
a 361
```

<210> 225

<211> 766

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 574, 610, 631, 643, 657, 660, 666, 688, 712, 735, 747

<223> n = A,T,C or G

<400> 225

```
agcgtgggtcg cgcccgaggt cctgtcagag tggcactggg agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgcct acattcggcg 180
ggatatggtc ttggcctatgc cttatggggg tggccggtgt gggcggtgtg gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caacactggg ttgctgacca gaagtgccag 300
gaagctgaat accatttcca gtgtcatacc cagggtgggt gacgaaagg gtcttttgaa 360
ctgtggaagg aacatccaag atctctggtc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctctgtc tttttccttc caatcagggg ctgctcttc tgattattct 480
tcagggaat gacataaatt gtatatcgg tcccggttcc aggccagtaa tagtagcctc 540
tgtgacacca gggcggggcc gagggaccct tctnttgaa gagaccagct tctcatactt 600
gatgatgagn ccgtaatcc tggcacgtgg nggttgcag atnccaccaa ggaaatnggn 660
ggggngggac ctgcccggcg gccgttcnaa agcccaattc cacacacttg gnggccgtac 720
tatggatccc actcngtcca acttgngnga atatggcata actttt 766
```

<210> 226

<211> 364

<212> DNA

<213> Homo sapiens

<400> 226

```
togagcggcc gcccgggcag gtccttgacc ttttcagcaa gtgggaagg gtaatccgtc 60
tccacagaca aggccaggac tcgtttgtag ccggtgatga tagaatggg tactgatgca 120
acagttgggt agccaatctg cagacagaca ctggcaacat tgccgacacc ctccaggaag 180
cgagaatgca gagtttcctc tgtgatatca agcacttcag ggttgtagat gctgccattg 240
tcgaacacct gctggatgac cagccaaaag gagaagggg agatgttgag catgttcagc 300
agcgtggctt cgctggctcc cactttgtct ccagtcttga tcagacctcg gccgcgacca 360
cgct 364
```

<210> 227
<211> 275
<212> DNA
<213> Homo sapiens

<400> 227
agcgtggtcg cggccgaggt ctgtcctaca gtcctcagga ctctactccc tcagcagcgt 60
ggtgaccgtg ccctccagca acttcggcac ccagacctac acctgcaacg tagatcacia 120
gcccagcaac accaaggttg acaagagagt tgagcccaaa tcttgtgaca aaactcacac 180
atgcccaccg tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccg 240
catccccctt ccaaacctgc ccgggcggcc gctcgt 275

<210> 228
<211> 275
<212> DNA
<213> Homo sapiens

<400> 228
cgagcggccg cccgggcagg tttggaaggg ggatgcgggg gaagaggaag actgacggtc 60
ccccaggag ttcaggtgct gggcacgggt ggcatgtgtg agttttgtca caagatttg 120
gtccaactct cttgtccacc ttggtgttgc tgggcttgtg atctacgttg caggtgtagg 180
tctgggtgcc gaagttgctg gagggcacgg tcaccacgct gctgagggag tagagtcttg 240
aggactgtag gacagacctc ggccgcgacc acgct 275

<210> 229
<211> 40
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 1, 4, 5, 13, 15, 17, 29
<223> n = A,T,C or G

<400> 229
nggnnggtcc ggnngnncag gaccactcnt cttcgaaata 40

<210> 230
<211> 208
<212> DNA
<213> Homo sapiens

<400> 230
agcgtggtcg cggccgaggt cctcaattgc ctctgcaaa gcaccgatag ctgcgctctg 60
gaagcgcaga tctgttttaa agtcctgagc aatttctcgc accagacgct ggaagggag 120
tttgcaatc agaagttcag tggaattctg ataacgtcta atttcacgga gcgccacagt 180
accaggacct gcccgggcgg ccgctcga 208

<210> 231
<211> 208
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 33
<223> n = A,T,C or G

<400> 231

```

tcgagcggcc gcccgggcag gtcctggtac tgnngcgctc cgtgaaatta gacgttatca 60
gaagtccact gaacttctga ttcgcaaact tcccttccag cgtctggtgc gagaaattgc 120
tcaggacttt aaaacagatc tgcgcttcca gagcgcagct atcggtgctt tgcaggaggc 180
aagtgaggac ctcggccgcg accacgct                                208

```

<210> 232

<211> 332

<212> DNA

<213> Homo sapiens

<400> 232

```

tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgt accagttctt ctgggccaca ctgggctgag tggggtacac gcagggtctca 180
ccagtctcca tgttgacagaa gactttgatg gcacccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcagggtgcgg 300
gcggggttct tgacctcggc cgcgaccacg ct                                332

```

<210> 233

<211> 415

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 6, 15, 19, 21

<223> n = A,T,C or G

<400> 233

```

gtgggnnttga acccnttttna nctccgcttg gtaccgagct cggatccact agtaacggcc 60
gccagtgtgc tggaaattcgg cttagcgtgg tcgcgggccga ggtcaagaac cccgcccgcga 120
cctgccgtga cctcaagatg tgccactctg actggaagag tggagagtac tggattgacc 180
ccaaccaagg ctgcaacctg gatgccatca aagtcttctg caacatggag actggtgaga 240
cctgccgtgta ccccaactcag cccagtgtgg ccagaagaa ctgggtacatc agcaagaacc 300
ccaaggacaa gaggcattgtc tggttcggcg agagcatgac cgatggattc cagttcgagt 360
atggcggcca gggctccgac cctgccgatg tggacctgcc cgggcggccg ctcga 415

```

<210> 234

<211> 776

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 505, 550, 574, 601, 604, 608, 612, 649, 656, 657, 680, 711, 750, 776

<223> n = A,T,C or G

<400> 234

```

agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagttagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa tttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagtg accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact gggtacagag taaccaccac tcccaaaaat 360
ggaccaggac caacaaaaac taaaactgca ggtccagatc aaacagaaat gactattgaa 420
ggcttgacgc ccacagtgga gtatgtggtt aagtgtctat gctcagaatc caagcggaga 480

```

```

gaagtcagcc tctggttcag actgnaagta accaacattg atcgccataa ggactggcat 540
tcactgatgn ggatgccgat tccatcaaaa ttgnttggga aaaccacacag gggcaagttt 600
ncangtcnag gnggacctac tcgagccctg aggatggaat ccttgactnt tccttinnct 660
gatggggaaa aaaaaccttn aaaacttgaa ggacctgccc gggcgggccgt ncaaaaccca 720
attccacccc cttgggggcg ttctatgggn cccactcgga ccaaacttgg ggtaan 776

```

<210> 235

<211> 805

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 637, 684, 705, 724, 733, 756, 778, 793, 796, 804

<223> n = A,T,C or G

<400> 235

```

tcgagcggcc gcccgggcag gtccttgacg ctctgcagtg tcttcttcac catcaggtgc 60
agggaaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg gcatccacat cagtgaatgc 180
cagtccttta gggcgatcaa tgttgggttac tgcagtctga accagaggct gactctctcc 240
gcttggtatc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt tttagttttt gttggtcctg gtccattttt 360
gggagtggtg gttactctgt aaccagtaac aggggaactt gaaggcagcc acttgacact 420
aatgctggtt tcctgaacat cggtcacttg catctgggat ggtttgtcaa tttctgttcg 480
gtaattaatg gaaattggct tgctgcttgc ggggcttgtc tccacggcca gtgacagcat 540
acacagtgat ggtataatca actccagggt taagccgctg atggtagctg aaactttgct 600
ccaggcacaa gtgaactcct gacagggcta tttcctnctg ttctccgtaa gtgatcctgt 660
aatatctcac tgggacagca ggagcattc caaaacttcg ggcgngaccc cctaagccga 720
attntgcaat atncatcaca ctggcgggcg ctcgancatt cattaaaagg cccaatcncc 780
cctataggga gtntantaca attng 805

```

<210> 236

<211> 262

<212> DNA

<213> Homo sapiens

<400> 236

```

tcgagcggcc gcccgggcag gtcaactttt gtttttggtc atgttcgggtt ggtcaaagat 60
aaaaactaag tttgagagat gaatgcaaag gaaaaaata ttttccaaag tccatgtgaa 120
attgtctccc attttttttg cttttgaggg ggttcagttt gggttgcttg tctgtttccg 180
ggttgggggg aaagttggtt gggtagggag gagccagggt gggatggagg gaggtttacg 240
gaagcagaca gggccaacgt cg 262

```

<210> 237

<211> 372

<212> DNA

<213> Homo sapiens

<400> 237

```

agcgtggtcg cggccgaggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60
ctgaaagacc agcagaggca taaggttcgg gaagagggtt ttaccgtggg caactctgtc 120
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttaggct ttggaagtgg tcatttcaga tgtgattcat ctataggttg ccatgacaat 300
gggtgtgaact acaagattgg agagaagtgg gaccgtcagg gagaaaatgg acctgcccg 360
gcggccgctc ga 372

```

<210> 238
<211> 372
<212> DNA
<213> Homo.sapiens

<400> 238
tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatccg taggttggtt 240
caagccttcg ttgacagagt tgcccacggg aacaacctct tcccgaacct tatgcctctg 300
ctggtctttc agtgccctcca ctatgatgtt gtaggtggca cctctggtga ggacctcggc 360
cgcgaccacg ct 372

<210> 239
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 478, 557, 563, 566, 620, 660, 663, 672, 673, 684, 693, 695
<223> n = A,T,C or G

<400> 239
tcgagcggcc gcccgggcag gtccaccata agtcctgata caaccacgga tgagctgtca 60
ggagcaagggt tgatttcttt catttggtccg gtcttctcct tgggggtcac ccgcactcga 120
tatccagtga gctgaacatt ggggtggtgtc cactgggcgc tcaggcttgt ggggtgtgacc 180
tgagtgaact tcaggtcagt tgggtgcagga atagtgggta ctgcagtctg aaccagaggc 240
tgactctctc cgcttgatt ctgagcatag aactaacca catactccac tgtgggctgc 300
aagccttcaa tagtcatttc tgtttgatct ggacctgcag ttttagtttt tgttggtcct 360
ggtccatttt tgggagtggt ggttactctg taaccagtaa cagggggaact tgaaggcagc 420
cacttgacac taatgctgtt gtcctgaaca tcggtcactt gcactctggga tggtttgnca 480
atctctgttc ggtaattaat ggaaattggc ttgctgcttg cggggctgtc tccacggcca 540
gtgacagcat acacagngat ggnatnatca actccaagtt taaggccctg atggtaactt 600
taaaacttgct ccagccagn gaacttccgg acagggtatt tcttctggtt ttccgaaagn 660
gancctggaa tnntctcctt ggancagaag gancntccaa aacttggggc ggaaccctt 720

<210> 240
<211> 691
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 564, 582, 640, 651, 666, 669, 690
<223> n = A,T,C or G

<400> 240
agcgtggtcg cggccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgtcct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgt gggcgggtgt gtccgcctaa 240
aaccatgttc ctcaaagatc atttggtgcc caacactggg ttgctgacca gaagtgccag 300
gaagctgaat acatttcca gtgtcatacc cagggtgggt gacgaaagg gtcttttgaa 360
ctgtggaagg aacatccaag atctctggtc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctctgtctgc ttttctcttc caatcagggg ctctctcttc tgattattct 480

```

tcagggcaat gacataaatt gtatatccgg ttcccgggtc caggccagta atagtagcct 540
cttgtgacac caggcggggc ccanggacca cttctctggg angagacca gcttctcata 600
cttgatgatg taaccggtg atcctgcacg tggcggctgn catgatacca ncaaggaatt 660
gggtgnggng gacctgcccg ggggcctcna a 691

```

<210> 241

<211> 808

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 680, 715, 721, 728, 735, 749, 757, 762, 772, 776, 779, 781, 792, 796, 800, 808

<223> n = A,T,C or G

<400> 241

```

agcgtgggtcg cggccgaggt ctgggatgct cctgctgtca cagtgaagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa ttccatttaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tccccaaaat 360
ggaccaggac caacaaaaac taaaactgca ggtccagatc aaacagaaat gactattgaa 420
ggcttgacgc ccacagtggg gtatgtgggt agtgtctatg ctccagaatcc aagcggagag 480
agtcagcctc tggttcagac tgcagtaacc actattcctg caccaactga cctgaagttc 540
actcaggtca caccacaag cctgagccgc cagtggacac caccatgt tcaactcactg 600
gatatcgagt gcgggtgacc cccaaggaga agaccggac ccatgaaaga aatcaacctt 660
gctcctgaca gctcatccgn gggtgtatca ggacttatgg gggactgccg cggcnggccg 720
ntcgaaancg aattntgaaa ttctcttcnc actggngggc gnttcgagct tncttntana 780
nggcccaatt cncctntagn gggtcgtn 808

```

<210> 242

<211> 26

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 22

<223> n = A,T,C or G

<400> 242

agcgtgggtcg cggccgaggt cnagga

26

<210> 243

<211> 697

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 496, 541, 624, 662, 679, 688

<223> n = A,T,C or G

<400> 243

```

tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctgggtatc atggcagccg 60
ccacgtgcca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120

```

```

gaagtgggtcc ctcggcccccg ccctgggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300
catggaccag agatcttgga tgttccttcc acagttcaaa agaccctttt cgtcaccac 360
cctgggtatg acactggaaa tgggtattcag cttcctggca cttctgggtca gcaaccag 420
gttgggcaac aaatgatctt tgaggaacat ggttttaggc ggaccacacc gccacaacg 480
ggcaccacca taaggatag gccaaagacca taccgcgcg aatgtaggac aagaagctct 540
ntctcaacaa ccatctcatg ggccccattc caggacactt ctgagtacat catttcatgt 600
catcctgggtg ggcaacttgat gaanaaccct tacagttcag ggttcctgga acttctacca 660
gngccacttc tgacagganc ttgggcgnga ccaccct 697

```

<210> 244

<211> 373

<212> DNA

<213> Homo sapiens

<400> 244

```

agcgtgggtcg cggccgaggt ccattttctc cctgacggtc ccacttctct ccaatcttgt 60
agtacacacc attgtcatgg caccatctag atgaatcaca tctgaaatga ccacttccaa 120
agcctaagca ctggcacaac agtttaaagc ctgattcaga cattcggtcc cactcatctc 180
caacggcata atgggaaact gtgtaggggt caaagcacga gtcattccgta ggttgggttca 240
agccttcgtt gacagagttg cccacggtaa caacctctt ccgaacctta tgcctctgct 300
ggtctttcag tgctccact atgatgttgt aggtggcacc tctggtgagg acctgcccgg 360
gcggcccgtc cga 373

```

<210> 245

<211> 307

<212> DNA

<213> Homo sapiens

<400> 245

```

agcgtgggtcg cggccgaggt gtgccccaga ccaggaattc ggcttcgacg ttggccctgt 60
ctgcttcctg taaactccct ccattcccaac ctggctccct cccacccaac caactttccc 120
cccaaccgg aaacagacaa gcaacccaaa ctgaaccccc tcaaaagcca aaaaaatggg 180
agacaatttc acatggactt tggaaaatat ttttttcctt tgcatcctc tctcaaaact 240
agtttttatc tttgaccaac cgaacatgac caaaaaccaa aagtgacctg cccggggcggc 300
cgctcga 307

```

<210> 246

<211> 372

<212> DNA

<213> Homo sapiens

<400> 246

```

tcgagcggcc gcccgggcag gtcctcacca gaggtgccac ctacaacatc atagtggagg 60
cactgaaaga ccagcagagg cataagggtt gggaagaggt tgttaccgtg ggcaactctg 120
tcaacgaagg cttgaaccaa cctacggatg actcgtgctt tgaccctac acagtttccc 180
attatgccgt tggagatgag tgggaacgaa tgtctgaatc aggttttaa ctgttggtgc 240
agtgccttag ctttggaggt ggtcatttca gatgtgattc atctagatgg tgccatgaca 300
atggtgtgaa ctacaagatt ggagagaagt gggaccgtca gggagaaaat ggacctcggc 360
cgcgaccag ct 372

```

<210> 247

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 284, 297, 299, 322, 325, 338, 342, 345

<223> n = A,T,C or G

<400> 247

```
tcgagcggcc gcccgggcag gtaccgggggt ggtcagcgag gagccattca cactgaactt 60
caccatcaac aacctgcggt atgaggagaa catgcagcac cctggctcca ggaagttcaa 120
caccacggag agggtccttc agggcctgct caggtccctg ttcaagagca ccagtgttgg 180
ccctctgtac tctggctgca gactgacttt gtcagacct gagaaacatg gggcagccac 240
tggagtggac gccatctgca ccctccgct tgatcccact ggtinctggac tggacanana 300
gcggctatac ttgggagctg anccnaacct ttggcgngga cncnctt 348
```

<210> 248

<211> 304

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 125

<223> n = A,T,C or G

<400> 248

```
gaggactggc tcagctccca gtatagccgc tctctgtcca gtccaggacc agtgggatca 60
aggcggaggg tgcagatggc gtccactcca gtggctgcc catgtttctc aagtctgagc 120
aaagncagtc tgcagccaga gtacagaggg ccaacactgg tgctcttgaa cagggacctg 180
agcaggccct gaaggaccct ctccgtggtg ttgaacttcc tggagccagg gtgctgcatg 240
ttctcctcat accgcagggt gttgatggtg aagttcagtg tgaatggctc ctgctgacc 300
accc 304
```

<210> 249

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 308, 310, 312, 320, 331, 336, 383, 392, 396

<223> n = A,T,C or G

<400> 249

```
agcgtggctg cggccgaggt ccaccacacc caattccttg ctggtatcat ggcagccgcc 60
acgtgccagg attaccggct acatcatcaa gtatgagaag cctgggtctc ctcccagaga 120
agtggctcct cggccccgcc ctggtgtcac agaggctact attactggcc tggaaaccggg 180
aaccgaatat acaatttatg tcattgccct gaagaataat cagaagagcg agcccctgat 240
tggaaaggaaa aagacagacg agcttcccca actggtaacc ctccacacc ccaatcttca 300
tggaccanan ancttggatn gtcctttcac nggttnaaaa aacccttttc gccccccac 360
cttgggggatt aaccttggga aanggggatt tnaccnttcc 400
```

<210> 250

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 338, 357, 361, 369, 388, 394

<223> n = A,T,C or G

```

<400> 250
tcgagcggcc gcccgggcag gtcctgtcag agtggcactg gtagaagttc caggaaccct 60
gaactgtaag ggttcttcat cagtccaac aggatgacat gaaatgatgt actcagaagt 120
gtcctggaat ggggcccatt agatggttgt ctgagagaga gcttcttgte ctacattcgg 180
cgggtatggt cttggcctat gccttatggg ggtggccggt gtgggcggtg tggtcgcct 240
aaaaccatgt tcctcaaaga tcatittgtt cccaacactg ggttgctgac cagaagtgcc 300
aggaagctga ataccatttc cagtgtcata cccaggngng gtgaccaaag ggggtcnttt 360
ngacctggng aaaggaacca tccaaaanct ctgncccatg 400

```

```

<210> 251
<211> 514
<212> .DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> 8, 107, 312, 338, 351, 352, 357, 363, 366, 373, 380, 405,
421, 444, 508
<223> n = A,T,C or G

```

```

<400> 251
agcgtggncg cggccgaggt ctgaggatgt aaactcttcc caggggaagg ctgaagtgtc 60
gaccatggtg ctactgggtc cttctgagtc agatatgtga ctgatngaa ctgaagtagg 120
tactgtagat ggtgaagtct. ggtgtccct aaatgctgca tctccagagc cttccatcat 180
taccgtttct tcttttgcta tgggatgaga cactgttgag tattctctaa agtcaccact 240
gaaatcttcc tccaaaggaa aacctgtgga aaagcccctt atttctgccc cataatttg 300
ttctcctaata cncctctgaaa tcactatttc cctggaangt ttgggaaaaa nngggcnacc 360
tgncantgga aantggatan aaagatccca ccattttacc caacnagcag aaagtgggaa 420
nggtaccgaa aagctccaag taanaaaaag gagggaaagta aaggtcaagt gggcaccagt 480
ttcaaacaaa actttcccca aactatanaa ccca 514

```

```

<210> 252
<211> 501
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> 20, 21, 25, 44, 343, 347, 356, 362, 387, 391, 398, 409, 428,
430, 453, 494
<223> n = A,T,C or G

```

```

<400> 252
aagcggccgc cggggcaggn ncagnagtgc cttcgggact gggntcacc cagggtctgc 60
ggcagttgtc acagcgccag ccccgctggc ctccaaagca tgtgcaggag caaatggcac 120
cgagatattc cttctgccac tgttctccta cgtggtatgt cttcccatca tcgtaacacg 180
ttgcctcatg agggtcacac ttgaattctc cttttccggt cccaagacat gtgcagctca 240
tttgcttggc tctatagttt ggggaaagtt tgttgaaact gtgccactga cttttacttc 300
ctccttctct actggagctt tccgtacctt ccacttctgc tgntggnaaa aaggngggaa 360
cntcttatca atttcattgg acagtanccc nctttctncc caaaacatnc aagggaat 420
attgattncn agagcggatt aaggaacaac ccnaattatg ggggccagaa ataaaggggg 480
ctttccaca ggtnttttcc t 501

```

```

<210> 253
<211> 226
<212> DNA
<213> Homo sapiens

```

<400> 253

```

tcgagcggcc gcccgggcag gtctgcaggc tattgtaagt gttctgagca catatgagat 60
aacctgggcc aagctatgat gtctgatacg ttaggtgtat taaatgact tttgactgcc 120
atctcagtg atgacagcct tctcactgac agcagagatc ttctcactg tgccagtggg 180
caggagaaa agcatgctgc gactggacct cggccgcgac cacgct 226

```

<210> 254

<211> 226

<212> DNA

<213> Homo sapiens

<400> 254

```

agcgtggtcg cggccgaggt ccagtcgcag catgctcttt ctctgccc a ctggcacagt 60
gaggaagatc tctgctgtca gtgagaaggc tgtcatccac tgagatggca gtcaaaagt 120
catttaatac acctaacgta tcgaacatca tagcttggcc caggttatct catatgtgct 180
cagaacactt acaatagcct gcagacctgc ccgggcggcc gctcga 226

```

<210> 255

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 327, 403

<223> n = A,T,C or G

<400> 255

```

cgagcggccg cccgggcaggt tccagactcc aatccagaga accaccaagc cagatgtcag 60
aagctacacc atcacaggtt tacaaccagg cactgactac aagatctacc tgtacacctt 120
gaatgacaat gctcggagct cccctgtggt catcgacgcc tccactgcca ttgatgcacc 180
atccaacctg cgtttccttg ccaccacacc caattccttg ctggtatcat ggcagccgcc 240
acgtgccagg attaccggt acatcatcaa gtatgagaag cctgggtctc ctcccagaga 300
agtggctccct cggccccgcc ctggtgncac agaagctact attactggcc tggaaaccggg 360
aaccgaatat acaatttatg tcattgccct gaagaataat canaagagcg agcccctgat 420
tggaagg 427

```

<210> 256

<211> 535

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 347, 456, 475

<223> n = A,T,C or G

<400> 256

```

agcgtggtcg cggccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atgggtgtct gagagagagc ttcttgcct gtctttttcc 180
ttccaatcag gggtcgcctc ttctgattat tcttcagggc aatgacataa attgtatatt 240
cggttcccgg ttccaggcca gtaatagtag cctctgtgac accagggcgg ggccgaggga 300
ccacttctct gggaggagac ccaggcttct catacttgat gatgtanccg gtaatcctgg 360
caccgtggcg gctgccatga taccagcaag gaattgggtg tgggtggcaa gaaacgcagg 420
ttggatggtg catcaatggc agtggaggcg tcgatnacca caggggagct ccgancattg 480
tcattcaagg tggacaggta gaatcttgta atcagggtgcc tggtttgtaa acctg 535

```

<210> 257
 <211> 544
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 495, 511
 <223> n = A,T,C or G

<400> 257
 tcgagcggcc gcccgggcag gtttcgtgac cgtgacctcg aggtggacac caccctcaag 60
 agcctgagcc agcagatcga gaacatccgg agcccagagg gcagccgcaa gaaccccgcc 120
 cgcacctgcc gtgacctcaa gatgtgccac tctgactgga agagtggaga gtactggatt 180
 gaccccaacc aaggctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggg 240
 gagacctgcg tgtaccccccac tcagcccaggt gtggcccaga agaactggta catcagcaag 300
 aaccccaagg acaagaagca tgtctgggtc gccgaaagca tgaccgatgg attccagttc 360
 gagtatggcg gccaggggtc cgaccctgcc gatgtggacc tcggccgcga ccacgctaag 420
 cccgaattcc agcacactgg cggccgttac tagtgggatc cgagcttcgg taccaagctt 480
 ggcgtaatca tgggncatag ctgtttcctg ngtgaaaatg gtattccgct tcacaatttc 540
 ccac 544

<210> 258
 <211> 418
 <212> DNA
 <213> Homo sapiens

<400> 258
 agcgtgggtcg cggccgaggt ccacatcggc agggctcggag ccctggccgc catactcgaa 60
 ctggaatcca tcggatcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
 gctgatgtac cagttcttct gggccacact gggtcagtg gggtacacgc aggtctcacc 180
 agtctccatg ttgcagaaga ctttgatggc atccagggtg cagccttggg tggggtaaat 240
 ccagtactct ccactcttcc agtcagagtg gcacatcttg aggtcacggc aggtgcgggc 300
 ggggttcttg cggctgccct ctgggtccg gatgttctcg atctgctggc tcaagctctt 360
 gaagggtggg gtccacctcg aggtcacggg cacgaaacct gcccgggcgg ccgctcga 418

<210> 259
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 320, 326, 342, 352
 <223> n = A,T,C or G

<400> 259
 agcgtgggtcg cggccgaggt caagaacccc gcccgcacct gccgtgacct caagatgtgc 60
 cactctgact ggaagagtgg agagtactgg attgaccca accaaggctg caacctggat 120
 gccatcaaag tcttctgcaa catggagact ggtgagacct gcgtgtacct cactcagccc 180
 agtgtggccc agaagaactg gtacatcagc aagaacccca aggacaagag gcatgtctgg 240
 ttcggcgaga gcatgaccga tggattccag ttcgagtatg gcggccaggg ctccgaccct 300
 gccgatgtgg acctgcccg gcccgnccgc tcgaaaagcc cnaatttcca gncacacttg 360
 gccggccggt actactg 377

<210> 260
 <211> 332

<212> DNA

<213> Homo sapiens

<400> 260

```

tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgt accagttctt ctggggccaca ctgggctgag tgggggtacac gcaggtctca 180
ccagtctcca tgttgacagaa gactttgatg gcatccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcaggtgcgg 300
gcgggggttct tgacctcggc cgcgaccacg ct                                     332

```

<210> 261

<211> 94

<212> DNA

<213> Homo sapiens

<400> 261

```

cgagcggccg cccgggcagg tccccccct ttttttttt ttttttttt ttttttttt 60
ttttttttt ttttttttt ttttttttt tttt                                     94

```

<210> 262

<211> 650

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 412, 582, 612, 641, 646

<223> n = A,T,C or G

<400> 262

```

agcgtggtcg cgcccgaggt ctggcattcc ttcgaattct ctccagccga gcttcccaga 60
acatcacata tcaactgcaaa aatagcattg catatcatgga tcaggccagt ggaaatgtaa 120
agaaggccct gaagctgatg gggtaaatg aaggtgaatt caaggctgaa ggaaatagca 180
aatcaccta cacagttctg gaggatggtt gcacgaaaca cactggggaa tggagcaaaa 240
cagtctttga atatcgaaca cgcaaggctg tgagactacc tattgtagat attgcaccct 300
atgacattgg tggctctgat caagaatttg gtgtggacgt tggccctggt tgctttttat 360
aaaccaaact ctatctgaaa tccaacaaa aaaaatttaa ctccatattg gntcctcttg 420
ttctaattct ggcaaccagt gcaagtgacc gacaaaattc cagttattta tttccaaaat 480
gtttggaaac agtataattt gacaaagaaa aaaggatact tctctttttt tggtctggtc 540
accaaataca attcaaaagg ctttttggtt ttattttttt anccaattcc aatttcaaaa 600
tgtctcaatg gngcttataa taaaataaac ttccaccctt ntttntgat 650

```

<210> 263

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 453, 458, 544

<223> n = A,T,C or G

<400> 263

```

agcgtggtcg cgcccgaggt ctgggatgct cctgctgtca cagttagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa tttccattaa ttaccgaaca 240

```

```

gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagaa gtaaccacca ctcccaaaaa 360
tggaccagga ccaacaaaaa ctaaaactgc aggtccagat caaacagaaa atggactatt 420
gaaggcttgc agcccacagt ggaagtatgt ggntaggngt ctatgctcag aatcccaagc 480
cggagaaagt cagccttctg gttagactg cagtaaccaa cattgatcgc cctaaaggac 540
tggnccattca cttggatggg ggatgtccaa ttc 573

```

<210> 264

<211> 550

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 39, 174, 352, 526

<223> n = A,T,C or G

<400> 264

```

tcgagcggcc gcccgggcag gtccttgacg ctctgcagng tcttcttcac catcaggtgc 60
agggaaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagngaattgc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttggattc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt ttaagtttt tgggtggcct gncctatttt 360
tgggaagtgg ggggttactc tgtaaccagt aacaggggaa cttgaaggca gccacttgac 420
actaatgctg ttgtcctgaa catcggtcac ttgcatctgg ggatggtttt gacaatttct 480
ggttcggaatc attaatggaa attggcttgc tgcttgccgg ggctgncctc acggggccagt 540
gacagcatac 550

```

<210> 265

<211> 596

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 347, 352, 353, 534, 555, 587

<223> n = A,T,C or G

<400> 265

```

tcgagcggcc gcccgggcag gtccttgacg ctctgcagtg tcttcttcac catcaggtgc 60
agggaaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagtgaattgc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttggattc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt ttaagtttt tgggtggcct gnnccatttt 360
tggggaaggg gtggttactc ttgtaaccag taacagggga acttgaagca gccacttgac 420
actaatgctg gtggcctgaa catcggtcac ttgcatctgg gatggtttgg tcaatttctg 480
ttcggtaattc aatgggaaat ttgcttactg gcttgccggg gctgtctcca cggncagtga 540
caagcataca caggngatgg gtataatcaa ctccagggtt aaggccnctg atggta 596

```

<210> 266

<211> 506

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 393, 473

<223> n = A,T,C or G

<400> 266

```

agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagtgaagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgaagc agtaagccaa tttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tcccaaaaat 360
gggaccagga ccaacaaaaa actaaaactg canggtccag atcaaacaga aatgactatt 420
gaaggcttgc agcccacagt ggagtatgtg ggtagtgtc tatgtcaga atnccaagcg 480
gagagagtca gcctctggtt cagact                                     506

```

<210> 267

<211> 548

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 346, 358, 432, 510, 512

<223> n = A,T,C or G

<400> 267

```

tcgagcggcc gcccgggcag gtcagcgctc tcaggacgtc accaccatgg cctgggctct 60
gtcctcctc accctcctca ctcagggcac agggctctgg gccagtcctg ccctgactca 120
gcctccctcc gcgtccgggt ctctctggaca gtcagtcacc atctcctgca ctggaaccag 180
cagtgcagtt ggtgcttatg aatttgcttc ctggtaccaa caacaccag gcaaggcccc 240
caaactcatg atttctgagg tactaagcg gccctcagg gtccctgatc gcttctctgg 300
ctccaagtct ggcaacacgg cctccctgac cgtctctggg ctccangctg aggatgangc 360
tgattattac tggaaagctca tatgcaggca acaacaattg ggtgttcggc ggaagggacc 420
aagctgaccg tnctaaggtc aagcccaagg cttgcccccc tcggtcactc tgttcccacc 480
ctcctctgaa gaagctttca agccaacaan gncacactgg gtgtgtctca taagtggact 540
ttctaccc                                     548

```

<210> 268

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 98, 380, 421, 454, 495, 506, 512, 561, 565, 579

<223> n = A,T,C or G

<400> 268

```

agcgtggtcg cggccgaggt ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc 60
tcaggtagct gctggccgcg tacttggtgt tgctttgntt ggaggggtgtg gtggtctcca 120
ctcccgctt gacggggctg ctatctgcct tccaggccac tgtcacggct cccgggtaga 180
agtcacttat gagacacacc agtgtggcct tgttggttg aagctcctca gaggaggtg 240
ggaacagagt gaccgagggg gcagccttgg gctgacctag gacggtcagc ttggtccctc 300
cgccgaacac ccaattgttg ttgcctgcat atgagctgca gtaataatca gcctcatcct 360
cagcctggag cccagagacn gtcaagggag gcccggtgtt gccaaagactt ggaagccaga 420
naagcgatca gggagccctg agggcgctt tacngacctc aaaaaatcat gaatttgggg 480
ggcctttgcc tggnggttgg ttggtnacca gnaaaacaaa atttcataaa gcaccaacgt 540
cactgctggt ttccagtgc ngaanatggt gaactgaant gtcc                                     584

```

<210> 269
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 265, 329
 <223> n = A,T,C or G

<400> 269
 agcgtggtcg cgcccgaggt ccagcatcag gagccccgcc ttgccggctc tggatcatgc 60
 ctttcttttt gtggcctgaa acgatgtcat caattcgag tagcagaact gccgtctcca 120
 ctgctgtctt ataagtctgc agcttcacag ccaatggctc ccatatgccc agttccttca 180
 tgtccaccaa agtaccgctc tcaccattta caccacaggt ctcacagttc tcctgggtgt 240
 gcttggcccc aagggaggta agtanacgga tgggtgctgg cccacagttc tggatcaggg 300
 tacgaggaat gacctctagg gcctgggcna caagccctgt atggacctgc ccgggcgggc 360
 ccgctcga 368

<210> 270
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 54, 163, 219, 229, 316
 <223> n = A,T,C or G

<400> 270
 tcgagcggcc gcccgggcag gtccatacag ggctgttgcc caggccctag aggnccattcc 60
 ttgtaccctg atccagaact gtgggaccag caccatccgt ctacttacct cccttcgggc 120
 caagcacacc caggagaact gtgagacctg ggtgtgaaat ggngagacgg gtacttttgt 180
 ggacatgaag gaactgggca tatgggagcc attggctgng aagctgcana cttataagac 240
 agcagtggag acggcagttc tgctactgag aattgatgac atcgtttcag gccacaaaaa 300
 gaaaggcgat gaccanagcc ggcaaggcgg ggcttctga tgctggacct cggccgccga 360
 ccacgctt 368

<210> 271
 <211> 424
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 279, 329, 362, 384, 400
 <223> n = A,T,C or G

<400> 271
 agcgtggtcg cgcccgaggt ccactagagg tctgtgtgcc attgcccagg cagagtctct 60
 gcgttacaaa ctccaggag ggcttgctgt gcggagggcc tgctatggtg tgctgcggtt 120
 catcatggag agtggggcca aaggctgcga ggtgtggtg tctgggaaac tccgaggaca 180
 gagggctaaa tccatgaagt ttgtggatgg cctgatgac cacagcggag accctgttaa 240
 ctactacgtt gacactgctg tgcgccacgt gttgctcana cagggtgtgc tgggcatcaa 300
 ggtgaagatc atgctgcctt gggacccanc tggcaaaaat ggcccttaaa aacccttgc 360
 cntgaccacg tgaaccattt gtngaaccc caagatgaan atacttgccc accaccccc 420
 attc 424

<210> 272
 <211> 541
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 422, 442, 510, 513, 515, 525
 <223> n = A,T,C or G

<400> 272
 tcgagcggcc gcccgggcag gtctgccaaag gagaccctgt tatgctgtgg ggactggctg 60
 gggcatggca ggcggctctg gcttcccacc cttctgttct gagatggggg tgggtgggcag 120
 tatctcatct ttgggttcca caatgctcac gtggtcaggc aggggettct tagggccaat 180
 cttaccagtt ggggtcccagg gcagcatgat cttcaccttg atgcccagca caccctgtct 240
 gagcaacacg tggcgcacag cagtgtcaac gtagtagtta acagggctct cgctgtggat 300
 catcaggcca tccacaaact tcatggattt agccctctgt cctcggagtt tcccaaaaca 360
 ccacaacctc gccagccttt gggccccact tcttcatgaa tgaaaccgca gcacaccatt 420
 ancaaggccc ttccgcacag gnaagccctt cctaaggagt tttgtaaacg caaaaaactc 480
 ttgcctgggg caaatgggca cacagacctn tantnggacc ttggnccgcg aaccaccgct 540
 t 541

<210> 273
 <211> 579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 223, 265, 277, 308, 329, 346, 360, 366, 429, 448, 517, 524,
 531, 578
 <223> n = A,T,C or G

<400> 273
 agcgtggctg cggccgaggt ctggccctcc tggcaaggct ggtgaagatg gtcaccctgg 60
 aaaacccgga cgacctggtg agagaggagt tggtggacca cagggtgctc gtggtttccc 120
 tggaaactct ggacttctct gcttcaaagg cattagggga cacaatggtc tggatggatt 180
 gaagggacag cccggtgctc ctggtgtgaa ggtgaacct gngccccctg gtgaaaatgg 240
 aactccaggt caaacaggag cccgngggct tcctgngag agaggacgtg ttggtgcccc 300
 tggcccanac ctgcccgggc ggccgctcna aaagccgaaa tccagnacac tggcggccgn 360
 tactantgga atccgaactt cggtaccaa gcttggccgt aatcatggcc atagcttgtt 420
 ccctgggng gaaattggta ttccgctncc aattccacac aacataccga acccgaaaag 480
 cattaaagtg taaaagccct gggggggcct aaatgangtg agcntaactc ncatttaatt 540
 ggcgttgccg ttcactgccc cgcttttcca gtccgggna 579

<210> 274
 <211> 330
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 171
 <223> n = A,T,C or G

<400> 274
 tcgagcggcc gcccgggcag gtctgggcca ggggcaccaa cacgtcctct ctcaccagga 60
 agccacagg ctctgtttg acctggagtt ccattttcac caggggcacc aggttcaccc 120

```

ttcacaccag gagcaccggg ctgtcccttc aatccatcca gaccattgtg ncccctaattg 180
cctttgaagc caggaagtcc aggagttcca gggaaaccac gagcaccctg tgggtccaaca 240
actcctctct caccaggctg tccgggtttt ccagggtgac catcttcacc agccttgcca 300
ggagggccag acctcggccg cgaccacgct                                     330

```

<210> 275

<211> 97

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 2, 35, 72

<223> n = A,T,C or G

<400> 275

```

ancgtggctg cgcccgaggt cctcaccaga ggtgncacct acaacatcat agtggaggca 60
ctgaaagacc ancagaggga taagggtcgg gaagagg                                     97

```

<210> 276

<211> 610

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 358, 360, 363, 382, 424, 433, 464, 468, 477, 491, 499, 511, 558, 584, 588, 590

<223> n = A,T,C or G

<400> 276

```

tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaattctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagttaaag gcctgattca gacattcggt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240
caagccttcg ttgacagagt tgtccacggg aacaacctct tcccgaacct tatgcctctg 300
ctggtctttc agtgccctca ctatgatgtt gtaggtggca cctctggtga ggacctcngn 360
ccngaacaac gcttaagccc gnattctgca gaataatccc atcacacttg gcggccgctt 420
cgancatgca tcntaaaagg ggcccccaatt tcccccttat aagngaancg gtatttncca 480
atttcactgg ncccgcgnt tttacaaacg ncggtgaact ggggaaaaac cctggcggtt 540
acccaacttt aatcgccntt ggcagcacia tcccccttt tcgnccancn tgggcgtaaa 600
taaccgaaaa                                     610

```

<210> 277

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 2, 5, 18, 21, 31

<223> n = A,T,C or G

<400> 277

```

ancgnggtcg cgcccgangt nttttttctt nttttttt

```

38

<210> 278

<211> 443

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 156, 212, 233, 245, 327, 331, 336, 361, 364, 381, 391, 397, 419, 437

<223> n = A,T,C or G

<400> 278

```

agcgtggtcg cgcccgaggt ctgaggttac atgcgtggtg gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gccgcggggag gagcagtaca acagcacgta ccgggnggtc agcgtcctca ccgtcctgca 180
ccagaattgg ttgaatggca aggagtacaa gngcaagggt tccaacaaag ccntcccagc 240
ccccntcgaa aaaaccattt ccaaagccaa agggcagccc cgagaaccac aggtgtacac 300
cctgccccca tcccgggagg aaaagancaa naaccnggtt cagccttaac ttgcttggtc 360
naangctttt tatcccaacg nacttcccc ntggaantgg gaaaaaccaa tgggccaanc 420
cgaaaaacaa ttacaanaac ccc                                     443

```

<210> 279

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 219, 256, 291, 297, 307, 314, 317

<223> n = A,T,C or G

<400> 279

```

tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtgggtc ttgtagttgt 60
tctccggctg cccattgctc tcccactcca cggcgatgtc gctgggatag aagcctttga 120
ccaggcaggt caggctgacc tggttcttgg tcatctctc cgggatggg ggcagggtga 180
acacctgggg ttctcggggc ttgccctttg gttttgaana tggttttctc gatgggggct 240
ggaagggtt ttgtgnaaac cttgcacttg actccttgcc attcaccag ncctggngca 300
ggacgngag gacnctnacc acacggaacc gggtggtgg actgetcc          348

```

<210> 280

<211> 149

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 18, 34, 51, 118, 120, 140

<223> n = A,T,C or G

<400> 280

```

agcgtggtcg cgacgangt cctgtcagag tggactggt agaagttcca ngaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagnn 120
cctggaatgg ggcccatgan atggttgcc                                     149

```

<210> 281

<211> 404

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
 <222> 383, 386, 388, 393
 <223> n = A,T,C or G

<400> 281
 tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctgggtatc atggcagccg 60
 ccacgtgccca ggattaccgg ctacatcadc aagtatgaga agcctgggtc tcctcccaga 120
 gaagtgggtcc ctcggccccg ccctgggtgc acagaggcta ctattactgg cctggaaccg 180
 ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240
 attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300
 catggaccag agatcttgga tgttccttcc acagttcaaa agaccccttt cggcaccccc 360
 cctgggtatg aacctgggaa aanggnantt aanccttctt ggca 404

<210> 282
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 320, 341, 424, 450, 459, 487, 498
 <223> n = A,T,C or G

<400> 282
 agcgtggctg cgcccgaggt ctgggatgct cctgctgtca cagtggagata ttacaggatc 60
 acttacggag aaacaggagg aaatagccct gtccaggagt tcactgtgcc tgggagcaag 120
 tctacagcta ccatcagcgg ccttaaaccct ggagttgatt ataccatcac tgtgtatgct 180
 gtcaactggcc gtgggagacag ccccgcaagc agcaagccaa ttccattaa ttaccgaaca 240
 gaaattgaca aaccatccca gatgcaagtg accgatgttc aggacaacag cattagtgtc 300
 aagtggctgc cttcaaggtn ccctgggtact gggttacaga ntaaccacca ctcccaaaaa 360
 tggaccagga accacaaaaa cttaactgc aggtgccaga tcaaacaga aatgactatt 420
 gaangcttgc agcccacagt gggagtatgn gggtagtgnc tatgcttcag aatccaagcg 480
 gaaaaangtc aagccttntg ggttcaa 507

<210> 283
 <211> 325
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 216, 292, 303, 304
 <223> n = A,T,C or G

<400> 283
 tcgagcggcc gcccgggcag gtccttgacg ctctgcagtg tcttcttcac catcagggtgc 60
 agggaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120
 ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagtgaatgc 180
 cagtccttta gggcgatcaa tgttggttac tgcagnctga accagaggct gactctctcc 240
 gcttggtatc tgagcataga cactaaccac atactccact gtgggctgca anccttcaat 300
 aanncatctt tgtttgatct ggacc 325

<210> 284
 <211> 331
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature

<222> 54, 59, 63, 121, 312, 327

<223> n = A,T,C or G

<400> 284

```
tcgagcggcc gcccgggcag gtctgggtgg gtcctggcac acgcacatgg gggngttgnt 60
ctnatccagc tgcccagccc ccattggcga gtttgagaag gtgtgcagca atgacaacaa 120
naccttcgac tcttctcgcc acttctttgc cacaaagtgc accctggagg gcaccaagaa 180
gggccacaag ctccacctgg actacatcgg gccttgcaaa tacatcccc cttgcctgga 240
ctctgagctg accgaattcc cccttgcgca tgcgggactg gctcaagaac cgtcctggca 300
cccttgtatg anagggatga agacacnacc c 331
```

<210> 285

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 316, 319, 327, 329, 339, 344, 357, 384, 398, 427, 443, 450, 478

<223> n = A,T,C or G

<400> 285

```
agcgtggctg cgcccgaggt ctgtcctaca gtcctcagga ctctactccc tcagcagcgt 60
ggtgaccgtg ccctccagca acttcggcac ccagacctac acctgcaacg tagatcacia 120
gccagcaac accaaggtgg acaagagagt tgagcccaaa tcttgtgaca aaactcacac 180
atgcccaccg tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccg 240
catccccctt ccaaacctgc ccggggcgcc gctcgaaagc cgaattccag cactctggcg 300
gccggtacta gtgganccna acttggnanc caacctggng gaantaatgg gcataantg 360
tttctggggg gaaattggta tccngtttac aattccnca caacatacga gccggaagca 420
taaaagngta aaagcctggg ggnggcctan tgaagtgaag ctaaactcac attaattngc 480
gttgccgctc actggcccgc ttttccagc 509
```

<210> 286

<211> 336

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 188, 251, 267

<223> n = A,T,C or G

<400> 286

```
tcgagcggcc gcccgggcag gtttggaagg gggatgcggg ggaagaggaa gactgacggt 60
ccccccagga gttcaggtgc tgggcacggg gggcatgtgt gagttttgtc acaagatttg 120
ggctcaactc tcttgtccac cttggtgttg ctgggcttgt gatctacgtt gcagggtgtag 180
gtctggngc cgaagttgct ggagggcacg gtcaccacgc tgctgagggg gtagagtcct 240
gaggactgta ngacagacct cggccgngac cacgctaagc cgaattctgc agatatccat 300
cacactggcg gccgctccga gcatgcattt tagagg 336
```

<210> 287

<211> 30

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
 <222> 8, 18
 <223> n = A,T,C or G

<400> 287
 agcgtggncg cggacganga caacaacccc

30

<210> 288
 <211> 316
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 22, 130
 <223> n = A,T,C or G

<400> 288
 tcgagcggcc gcccgggcag gnccacatcg gcagggtcgg agccctggcc gccatactcg 60
 aactggaatc catcggtcat gctottgccg aaccagacat gcctcttgct cttgggggttc 120
 ttgctgatgn accagttctt ctggggccaca ctgggctgag tgggggtacac gcagggtctca 180
 ccagttctcca tgttgcagaa gactttgatg gcattccaggt tgcagccttg gttgggggtca 240
 atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcagggtgcgg 300
 gcgggggttct tgacct 316

<210> 289
 <211> 308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 36, 165, 191, 195, 218, 235
 <223> n = A,T,C or G

<400> 289
 agcgtggctg cggccgaggt ccagcctgga gataanggtg aagggtggtgc ccccggaactt 60
 ccaggatatag ctggacctcg tggtagccct ggtgagagag gtgaaactgg ccctccagga 120
 cctgctggtt tccctggtgc tcctggacag aatggtgaac ctggnggtaa aggagaaaga 180
 ggggctccgg ntganaaagg tgaaggaggc cctcctgnat tggcaggggc cccangactt 240
 agagggtggag ctggccccc tggcccccga ggaggaaagg gtgctgctgg tcctcctggg 300
 ccacctgg 308

<210> 290
 <211> 324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 184
 <223> n = A,T,C or G

<400> 290
 tcgagcggcc gcccgggcag gtctgggcca ggaggaccaa taggaccagt aggaccctt 60
 gggccatctt tccctgggac accatcagca cctggaccgc ctgggtcacc cttgtcaccc 120
 tttggaccag gacttccaag acctcctctt tctccaggca ttccttgca accaggagta 180
 ccancagcac caggtggccc aggaggacca gcagcacctt ttcctccttc gggaccaggg 240

ggaccagctc cacctctaag tcttggggcc cctgccaatc caggagggcc tccttcacct 300
 ttctcaccgc gagccctctt ttct 324

<210> 291
 <211> 278
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 249, 267
 <223> n = A,T,C or G

<400> 291
 tcgagcggcc gcccgggcag gtccaccggg atattcgggg gtctggcagg aatgggaggc 60
 atccagaacg agaaggagac catgcaaagc ctgaacgacc gcctggcctc ttacctggac 120
 agagtgagga gcctggagac cgacaaccgg aggctggaga gcaaaatccg ggagcacttg 180
 gagaagaagg gaccccaggt cagagactgg agccattact tcaagatcat cgaggacctg 240
 agggctcana tcttcgcaaa tactgcngac aatgcccg 278

<210> 292
 <211> 299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 6, 19, 25, 51, 53, 61, 63, 70, 109, 136, 157, 241, 276
 <223> n = A,T,C or G

<400> 292
 atgcgnggtc gcggccgang accanctctg gctcatactt gactctaaag ncntcaccag 60
 nanttacggn cattgccaat ctgcagaacg atgcgggcat tgtccgcant atttgccaag 120
 atctgagccc tcaggncctc gatgatcttg aagtaanggc tccagtctct gacctggggg 180
 cccttcttct ccaagtgtc ccgattttg ctctccagcc tccggttctc ggtctccaag 240
 ncttctcact ctgtccagga aaagaggcca ggcgngcgat cagggtttt gcatggact 299

<210> 293
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 293
 agcgtgggtc cgcccgaggt tgtacaagct tttttttttt tttttttttt tttttttttt 60
 tttttttttt tttttttttt tttttttttt tttttttttt t 101

<210> 294
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 64, 103, 110, 237, 282
 <223> n = A,T,C or G

<400> 294
 tcgagcggcc gcccgggcag gtctgccaac accaagattg gccccgccg catccacaca 60

```

gttngtgtgc ggggaggtaa caagaaatac cgtgccctga ggntggacgn ggggaatttc 120
tcctggggct cagagtgttg tactcgtaaa acaaggatca tcgatgttgt ctacaatgca 180
tctaataacg agctggttcg taccaagacc ctggtgaaga attgcatcgt gctcatngac 240
agcacaccgt accgacagtg ggtaccgaag tcccactatg cncct 285

```

<210> 295

<211> 216

<212> DNA

<213> Homo sapiens

<400> 295

```

tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggatc atggcagccg 60
ccacgtggcca cgattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtggtec ctcggccccg ccctgggtgc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaag 216

```

<210> 296

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 7, 10, 33, 61, 62, 63, 88, 109, 122, 255, 298, 307, 340, 355, 386, 393

<223> n = A,T,C or G

<400> 296

```

agcgtgntcn cgcccgagga tggggaagct cgncgtgtctt tttccttcca atcaggggct 60
nnntcttctg attattcttc agggcaanga cataaattgt atattcggnt cccgggtcca 120
gnccagtaat agtagcctct gtgacaccag ggcggggccg agggaccact tctctgggag 180
gagacccagg cttctcatac ttgatgatga agccggtaat cctggcacgt ggcgggctgc 240
catgatacca ccaangaatt ggggtgtggtg gacctgcccg ggcggggccg tcgaaaancc 300
gaattcntgc aagaatatcc atcacacttg ggcggggccg tcgaaccatg catcntaaaa 360
gggccccaat ttcccccta ttaggngaag cncatttaa caaattccac ttgg 414

```

<210> 297

<211> 376

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 312, 326, 335, 361

<223> n = A,T,C or G

<400> 297

```

tcgagcggcc gcccgggcag gtctcgcggt cgcactggtg atgctgggtc tgttgggtccc 60
cccgccctc ctggacctcc tggctcccct ggtcctccca gcgctgggtt cgacttcagc 120
ttcctgcccc agccacctca agagaaggct cacgatggtg gccgctacta ccgggctgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagccttgag 240
ccagcagaat cgaaaacatt cggaacccaa gaagggaag cccgcaaaga aaccccgccc 300
gcacctggcc gngaacctcc aagaangtgc ccacntcttg actgggaaaa aaagggaana 360
ntacttgga ttggac 376

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<210> 298

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 345, 346

<223> n = A,T,C or G

<400> 298

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ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtacacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggttg cagccttggt tggggccaat 240
ccagtactct ccactcttcc agtcagaagt ggcacatctt gaggtcacgg caggggtcgg 300
gcgggggttct tgcgggctgc cttctgggc tcccgaatg ttctnngaac ttgctgg 357
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<210> 299

<211> 307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 281, 285, 306

<223> n = A,T,C or G

<400> 299

```
agcgtggtcg cggccgaggt ccactagagg tctgtgtgcc attgcccagg cagagtctct 60
gcgttacaaa ctccctaggag ggcttgctgt gcggagggcc tgctatggtg tgctgcggtt 120
catcatggag agtggggcca aaggctgcga ggttggtgtg tctgggaaac tccgaggaca 180
gagggctaaa tccatgaagt ttgtggatgg cctgatgatc cacagcggag accctgttaa 240
ctactacgtt gacacttgct tgtgcgccac gtgttgctca nacanggggtg ggctgggcat 300
caaggng 307
```

<210> 300

<211> 351

<212> DNA

<213> Homo sapiens

<400> 300

```
tcgagcggcc gcccgggcag gtctgccaag gagaccctgt tatgctgtgg ggactggctg 60
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tatctcatct ttgggttcca caatgctcac gtggtcaggc aggggcttct tagggccaat 180
cttaccagtt ggggtcccagg gcagcatgat cttcaccttg atgcccagca caccctgtct 240
gagcaacacg tggcgcacag caagtgtcaa cgtaagtaag ttaacagggt ctccgctgtg 300
gatcatcagg ccatccacaa acttcatgga ttaaccctc tgtcctcgga g 351
```

<210> 301

<211> 330

<212> DNA

<213> Homo sapiens

<400> 301

```
tcgagcggcc gcccgggcag gtgtttcaga ggttccaagg tccactgtgg aggtcccagg 60
agtgtgtgtg gtgggcacag aggtccgatg ggtgaaacca ttgacataga gactgttctt 120
gtccagggtg taggggccca gctctttgat gccattggcc agttggctca gctcccagta 180
cagccgctct ctgtttgagtc cagggctttt ggggtcaaga tgatggatgc agatggcatc 240
cactccagtg gctgtccat ccttctcgga cctgagagag gtcagtctgc agccagagta 300
cagagggcca acactggtgt tctttgaata 330
```

<210> 302
 <211> 317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 129, 295
 <223> n = A,T,C or G

<400> 302
 agcgtggtcg cgcccgaggt ctgtactggg agctaagcaa actgaccaat gacattgaag 60
 agctgggccc ctacaccctg gacaggaaca gtctctatgt caatggtttc acccatcaga 120
 gctctgtgnc caccaccagc actcctggga cctccacagt ggatttcaga acctcaggga 180
 ctccatcctc cctctccagc cccacaatta tggctgctgg ccctctcctg gtaccattca 240
 ccctcaactt caccatcacc aacctgcagt atggggagga catgggtcac cctgnctcca 300
 ggaagttcaa caccaca 317

<210> 303
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 139, 146, 195
 <223> n = A,T,C or G

<400> 303
 tcgagcggcc gcccgacag gtctgggcgg atagcaccgg gcatattttg gaatggatga 60
 ggtctggcac cctgagcagt ccagcgagga ctgtgtctta gttgagcaat ttggctagga 120
 ggatagtatg cagcaccgnt ctgagncgtg gggatagctg ccatgaagta acctgaagga 180
 ggtgctggct ggtanggggt gattacaggg ttgggaacag ctcgtaact tgccattctc 240
 tgcataact ggtagtgag gtgagcctgg ccctcttctt ttg 283

<210> 304
 <211> 72
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 59
 <223> n = A,T,C or G

<400> 304
 agcgtggtcg cgcccgaggt gagccacagg tgaccggggc tgaagctggg gctgctggnc 60
 ctgctggtcc tg 72

<210> 305
 <211> 245
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 5, 11, 22, 98, 102

<223> n = A,T,C or G

<400> 305

```
cagcngctcc nacggggcct gngggaccaa caacaccgtt ttcaccctta ggccctttgg 60
ctcctctttc tccttttagc ccagggttgac cagcagcncc ancaggacca gcaaattccat 120
tggggccagc aggaccgacc tcaccacgtt caccagggct tcccgcagga ccagcaggac 180
cagcaggacc agcagcccca gtttcgcccc ggtcacctgt ggctcacctc ggccgcgacc 240
acgct 245
```

<210> 306

<211> 246

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 144, 159

<223> n = A,T,C or G

<400> 306

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tcgagcggtc gcccgggcag gtccaccggg atagccgggg gtctggcagg aatgggaggc 60
atccagaacg agaaggagac catgcaaagc ctgaacgacc gcctggcctc ttacctggac 120
agagtgagga gcctggagac cganaaccgg aggtggana gcaaatccg ggagcacttg 180
gagaagaagg gaccccaggt caagagactg gagccattac ttcaagatca tcgagggacc 240
tgaggg 246
```

<210> 307

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 5

<223> n = A,T,C or G

<400> 307

```
agcngngtcg cgcccgaggt ccagctctgt ctcatatttg actctaaagt catcagcagc 60
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ctgagccctc aggtcctcga tgatcttgaa gtaatggctc cagtctctga cctgggggtcc 180
cttcttctcc aagtgtctcc ggattttgct ctccagcctc cggttctcgg tctccaggct 240
cctcactctg tccaggtaag aaggcccagg cggtcgttca ggctttgcat ggtctccttc 300
tcgttctgga tgcttcccat tcctgccaga ccc 333
```

<210> 308

<211> 310

<212> DNA

<213> Homo sapiens

<400> 308

```
tcgagcggcc gcccgggcag gtcaggaagc acattgggtct tagagccact gcctcctgga 60
ttccacctgt gctgcggaca tctccaggga gtgcagaagg gaagcaggtc aaactgctca 120
gatcagtcag actggctggt ctcatgtctc acctgagcaa ggtagtctg cagccagagt 180
acagagggcc aacctgggtg ttcttgaaca agggcttgag cagaccctgc agaaccctct 240
tccgtggtgt tgaacttcct ggaaaccagg gtgttgcatt ttttctctca taatgcaagg 300
ttggtgatgg 310
```

<210> 309

<211> 429

<212> DNA

<213> Homo sapiens

<400> 309

```

agcgtggtcg cgcccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgtcct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagaccg caggctctac 180
cagtctccat gttgcagaag actttgatgg catccagggt gcagccttgg ttgggggtcaa 240
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cgggcccggg gttcttgccg cttgccctct gggctccgga tgttctcgat ctgcttggct 360
caggctcttg agggtggggtg tccacctcga ggtcacggtc accgaaacct gcccgggcg 420
ccgctcga                                     429

```

<210> 310

<211> 430

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 342

<223> n = A,T,C or G

<400> 310

```

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ccagtttcga gtattggcgg ccagggtctt ccgaccttg ccgatgtgga cctcggccgc 420
gaccaccgct                                     430

```

<210> 311

<211> 2996

<212> DNA

<213> Homo sapiens

<400> 311

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cagccaccgg agtggatgcc atctgcaccc accgccctga cccacagggc cctgggctgg 60
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cctacaccct ggacagggac agtctctatg tcaatggttt cacacagcgg agctctgtgc 180
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```

```

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<210> 312

<211> 914

<212> PRT

<213> Homo sapiens

<400> 312

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Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
65          70          75          80
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
85          90          95
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
100         105         110
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
115         120         125
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
130         135         140
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr

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145					150				155				160			
His	Arg	Ser	Ser	Val	Ser	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Val	
				165					170				175			
Tyr	Leu	Gly	Ala	Ser	Lys	Thr	Pro	Ala	Ser	Ile	Phe	Gly	Pro	Ser	Ala	
				180					185				190			
Ala	Ser	His	Leu	Leu	Ile	Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	
				195					200				205			
Leu	Arg	Tyr	Glu	Glu	Asn	Met	Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	
				210					215				220			
Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	
				225					230				235			
Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	
				245					250				255			
Glu	Lys	Asp	Gly	Glu	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	
				260					265				270			
Pro	Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Leu	Glu	
				275					280				285			
Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	
				290					295				300			
Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	
				305					310				315			
Pro	Thr	Thr	Ser	Thr	Gly	Val	Val	Ser	Glu	Glu	Pro	Phe	Thr	Leu	Asn	
				325					330				335			
Phe	Thr	Ile	Asn	Asn	Leu	Arg	Tyr	Met	Ala	Asp	Met	Gly	Gln	Pro	Gly	
				340					345				350			
Ser	Leu	Lys	Phe	Asn	Ile	Thr	Asp	Asn	Val	Met	Lys	His	Leu	Leu	Ser	
				355					360				365			
Pro	Leu	Phe	Gln	Arg	Ser	Ser	Leu	Gly	Ala	Arg	Tyr	Thr	Gly	Cys	Arg	
				370					375				380			
Val	Ile	Ala	Leu	Arg	Ser	Val	Lys	Asn	Gly	Ala	Glu	Thr	Arg	Val	Asp	
				385					390				395			
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				405					410				415			
Lys	Gln	Val	Phe	His	Glu	Leu	Ser	Gln	Gln	Thr	His	Gly	Ile	Thr	Arg	
				420					425				430			
Leu	Gly	Pro	Tyr	Ser	Leu	Asp	Lys	Asp	Ser	Leu	Tyr	Leu	Asn	Gly	Tyr	
				435					440				445			
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				450					455				460			
Thr	Phe	Leu	Pro	Pro	Leu	Ser	Glu	Ala	Thr	Thr	Ala	Met	Gly	Tyr	His	
				465					470				475			
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				485					490				495			
Pro	Asp	Met	Gly	Lys	Gly	Ser	Ala	Thr	Phe	Asn	Ser	Thr	Glu	Gly	Val	
				500					505				510			
Leu	Gln	His	Leu	Leu	Arg	Pro	Leu	Phe	Gln	Lys	Ser	Ser	Met	Gly	Pro	
				515					520				525			
Phe	Tyr	Leu	Gly	Cys	Gln	Leu	Ile	Ser	Leu	Arg	Pro	Glu	Lys	Asp	Gly	
				530					535				540			
Ala	Ala	Thr	Gly	Val	Asp	Thr	Thr	Cys	Thr	Tyr	His	Pro	Asp	Pro	Val	
				545					550				555			
Gly	Pro	Gly	Leu	Asp	Ile	Gln	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	
				565					570				575			
Thr	His	Gly	Val	Thr	Gln	Leu	Gly	Phe	Tyr	Val	Leu	Asp				

610	615	620
Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys		
625	630	635
Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe		
	645	650
Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys		
	660	665
Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe		
	675	680
Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr		
	690	695
Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln		
705	710	715
Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile		
	725	730
Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn		
	740	745
Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe		
	755	760
Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr		
	770	775
Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys		
785	790	795
Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu		
	805	810
Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr		
	820	825
Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn		
	835	840
Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu		
	850	855
Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly		
865	870	875
Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val		
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Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp		
	900	905
Leu Gln		910

<210> 313

<211> 656

<212> DNA

<213> Homo sapiens

<400> 313

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```

<210> 314
 <211> 519
 <212> DNA
 <213> Homo sapiens

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 gtttaaggat ggtctcggtg gttaggccca ctagaataaa ctgagtccaa tacctctaca 180
 cagttatgtt taactgggct ctctgacacc gggaggaagg tggcgggggt taggtgttgc 240
 aaacttcaat ggttatgcgg ggatgttcac agagcaagct ttggtatcta gctagtctag 300
 cattcattag ctaatgggtg cctttgggtat ttattaaaat caccacagca tagggggact 360
 ttatgttttag gttttgtcta agagttagct tatctgcttc ttgtgctaac agggctattg 420
 ctaccaggga ctttggacat gggggccagc gtttggaac ctcatctagt ttttttgaga 480
 gataggccac tggccttgga ctcggccgc gaccacgct 519

<210> 315
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 315
 cacagagcgt ttattgacac caccactcct gaaaattggg atttcttatt aggttcccct 60
 aaaagttccc atgttgatta catgtaaata gtcacatata tacaatgaag gcagtttctt 120
 cagaggcaac cagggtttat agtgctaggt aaatgtcatc tcttttgtgc tactgactca 180
 ttgtcaaacg tctctgcact gttttcagcc tctccacgtt gcctctgtcc tgcttcttag 240
 ttccttcttt gtgacaaacc aaaagaataa gaggatttag aacaggactg cttttcccct 300
 atgattttaa aattccaatg actttcgccc ttgggagaaa tttccaagga aatctctctc 360
 gctcgctctc tccgttttcc tttgtgagct tctgggggag ggtagtggt gactttttga 420
 tacgaaaaaa tgcattttgt g 441

<210> 316
 <211> 247
 <212> DNA
 <213> Homo sapiens

<400> 316
 tggcgoggct gctggatttc accttcttgc acctgccggt gagcgccctg ggtctaaagg 60
 ggcgggatac tccattatgg cccctcgccc tgtagggctg gaatagttag aaaaggcaac 120
 ccagtctagc ttggtaagaa gagagacatg ccccaaacct cggcgccctt ttctctcag 180
 atctgctgtc cttacttcag cgactgcagg agcttcacct gcaagaaaac agcattgagc 240
 tgctgac 247

<210> 317
 <211> 409
 <212> DNA
 <213> Homo sapiens

<400> 317
 tgacagggct cctggagttg ttaagtcacc aagtagctgc aggggatgga cactgcccc 60
 cacgatgtgg gatgaacagc agccttgggt ttagagccag ggtgtccatg gatttgacct 120
 gaatgctccc tggaggccct gtggcgagga caggcactgg atggtccaga ccctctggct 180
 ggaggagtgg tggagccagg actgggcctt cagccatgag ggctagaata acctgacctc 240
 ttgcattcta acactgggtc attaatgaca cctttccagt ggatgttgca aaaaccaaca 300
 ctgtcaggaa cctggccctg ggagggtcga ggtgagctca caaggagagg tcaagccaag 360
 ccaaagggta ggkaacacac aacaccaggg gaaaccagcc cccaaacca 409

<210> 318
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 6, 17, 24, 271
<223> n = A,T,C or G

<400> 318
caaggnagat cttaagnggg gtcntatgta agtgtgctcc tggctccagg gttcctggag 60
cctcacgagg tcaggggaac cctttagtaa ctccaccagc agcatcatct cgtgaaggat 120
gtcattgggtc aggaagctgt cctggacgta ggccatctcc acatccatgg ggatgccata 180
gtcactgggc ctttgctcgg gaggaggcat caccagaaa ggcgagatct tggactcggg 240
gcctgggttg ccagaatagt aaggggagca naggcaggcg aggcagggct ggaagccatt 300
gctggagccc tgcagccgca 320

<210> 319
<211> 212
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 172
<223> n = A,T,C or G

<400> 319
tgaagcaata gcgccccat tttacaggcg gagcatggaa gccagagagg tgggtggggg 60
aggggggtcct tccctggctc aggcagatgg gaagatgagg aagccgctga agacgctgtc 120
ggcctcagag ccctggtaaa tgtgaccctt tttgggggtct ttttcaacct anacctgtgc 180
accctgctgc agacctcggc cgcgaccacg ct 212

<210> 320
<211> 769
<212> DNA
<213> Homo sapiens

<400> 320
tggagggtgta gcagtgagag gagatytcag gcaagagtgt cacagcagag ccctaaascc 60
tccaactcac cagtgagaga tgagactgcc cagtactcag ccttcatctc ctggggccacc 120
tggaggggcgt ctttctccat cagcgcatac tgagcagggg tactcagatc cttcttggaa 180
cctacaagga agagaagcac actggaaggg tcattctcct tcagggcatc ggccagccac 240
tgccctgccat gggagggtgga aagtaaggga tgagttagtc tgcagggccc ctcccactga 300
cattcatagg cccaattacc ccctctctgg tctacatgc attcttcttc ttcctgacca 360
cccctctgtt ctgaacctc tcttcccga gcctccatt atattgcagg atgctcactt 420
acttggtatg ttccagagat gccacatcat tcagggtgaa gacaatgatg atggcttgga 480
agagtggcag aaacagcccc aggttgacag ggaagacact actgctcatt tccccaatcc 540
ttccagctcc atatgagaaa gccatgtgca ctctgagacc cacctacccc acttcaccca 600
gccccttacc ttgagctcct ctatagtagg ttgatgcaat gcatttgaac ctctcctgcc 660
cagcggtatc ccaactggaa ggaaggaaga gtgaagcaca ggtatgtatc ttgggggggtg 720
tgggtgctgg ggagaaggga tagctggaag ggggtgtgaa gcactcaca 769

<210> 321
<211> 690
<212> DNA
<213> Homo sapiens

<220>
 <221> misc_feature
 <222> 633, 666
 <223> n = A,T,C or G

<400> 321
 tgggctgtgg gcggcacctg tgctctgcag gccagacagc gatagaagcc tttgtctgtg 60
 cctactcccc cggaggcaac tgggaggtca acggaagac aatcatcccc tataagaagg 120
 gtgcctggtg ttcgctctgc acagccagtg tctcaggctg cttcaaagcc tgggaccatg 180
 caggggggct ctgtgaggtc cccaggaatc cttgtcgcat gagctgccag aaccatggac 240
 gtctcaacat cagcacctgc cactgccact gtccccctgg ctacacgggc agatactgcc 300
 aagtgaggtg cagcctgcag tgtgtgcacg gccggttccg ggaggaggag tgctcgtgcg 360
 tctgtgacat cggctacggg ggagcccagt gtgccaccaa ggtgcatttt cccttcacaa 420
 cctgtgacct gaggatcgac ggagactgct tcatggtgtc ttcagaggca gacacctatt 480
 acagaagcca ggatgaaatg tcagagggaat gccggggtgc tggcccagat caagagccag 540
 aaagtgcagg acatcctcgc cttctatctg gccgcctgg agaccaccaa cgagggtgact 600
 gacagtgact ttgagaccag gaacttctgg atnngggtca cctacaagac cgccaaggac 660
 tccttncgct gggccacagc ggagcaccag 690

<210> 322
 <211> 104
 <212> DNA
 <213> Homo sapiens

<400> 322
 gtcgcaagcc ggagcaccac catgtagcct ttcccgaagt accggacctt ctctcctccc 60
 acgctcacat cacggacatc atggagcagg accaccacct ggtc 104

<210> 323
 <211> 118
 <212> DNA
 <213> Homo sapiens

<400> 323
 gggccctggg cgcttccaaa tgacccagga ggtggtctgc gacgaatgcc ctaatgtcaa 60
 actagtgaat gaagaacgaa cactggaagt agaaatagag cctgggggtga gagacgga 118

<210> 324
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 324
 tgctctccgg gagcttgaag aagaaactgg ctacaaaggg gacattgccg aatgtttctcc 60
 agcgggtctgt. atggacccag gcttgtcaaa ctgtactata cacatcgtga cagtcaccat 120
 taacggagat gatgccgaaa acgcaaggcc gaagccaaag ccaggggatg gagagtttgt 180
 ggaagtcatt tctttaccca agaatgacct gctgcagaga cttgatgctc tggtagctga 240
 agaacatctc acagtggacg ccagggtcta ttcctacgct ctacgctga aacatgcaaa 300
 tgcaaaagcca tttgaagtgc cttctttgaa attttaagcc caaatatgac actg 354

<210> 325
 <211> 642
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> 1

<223> n = A,T,C or G

<400> 325

```
ncatgcttga atgggctcct ggtgagagat tgccccctgg tggtgaaaca atcgtgtgtg 60
cccactgata ccaagaccaa tgaaagagac acagttaagc agcaatccat ctcatattcca 120
ggcacttcaa taggtcgctg attggtcctt gcaccagcag tggtagtcgt acctatttca 180
gagaggtctg aaattcaggt tcttagtttg ccagggacag gccctacctt atattttttt 240
ccatcttcat catccacttc tgcttacagt ttgctgctta caataactta atgatggatt 300
gagttatctg ggtggtctct agccatctgg gcagtgtggt tctgtctaac caaagggcat 360
tggcctcaaa ccctgcattt ggtttagggg ctaacagagc tcctcagata atcttcacac 420
acatgtaact gctggagatc ttattctatt atgaataaga aacgagaagt ttttccaaag 480
tgttagtcag gatctgaagg ctgtcattca gataaccag cttttccttt tggcttttag 540
cccattcaga ctttgccaga gtcaagccaa ggattgcttt tttgctacag ttttctgcc 600
aatggcctag ttcttgagta cctggaaacc agagagaaag ag 642
```

<210> 326

<211> 455

<212> DNA

<213> Homo sapiens

<400> 326

```
tccgtgagga tgagcttga gtccttcacc aggcactgca ggggcacagt cacgtcaatc 60
accttcacct tctcgctctt cctgctcttg tcattgacaa acttcccgta ccaggcattg 120
acgatgatga ggccattctt ggactcttct gcctcaatta tccttcggac agattcctgc 180
atcagccgga cagcggactc cgctcttgca ttcttctgca gcacatcggg gccggcgctt 240
tccctctgct tctccaattc cttctctttc tgagccctga ggtatggttt gatgatcaga 300
cgggtgcatgg caaagtagac cactagaggg ccacgggtgg catagaacat gccgctgggc 360
agaagctggg ccgtcaagtg aatagggaag aagtatgtct gactggccct gttgagcttg 420
actttgagag aaacgcctg tggaactcca acgct 455
```

<210> 327

<211> 321

<212> DNA

<213> Homo sapiens

<400> 327

```
ttcactgtga actcgcagtc ctcgatgaac tcgcacagat gtgacagccc tgtctccttg 60
ctctctgagt tctcttcaat gatgctgatg atgcagtcga cgatagcgcg cttataactca 120
aagccaccct cttcccgag catggtgaac aggaagttca taaggacggc gtgtttgcga 180
ggatatttct gacacagggc actgatggcc tggacaacca ccaccttgaa ttcattccag 240
atttctgaca tgaaggagga gatctgcttc atgaggcggt cgatgctgct ctgctgccc 300
gtcttaagga ggggtggtgat g 321
```

<210> 328

<211> 476

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 302, 311

<223> n = A,T,C or G

<400> 328

```
tgcaggaggg gccatggggg ctgtgaatgg gatgcagccc catggtgtcc ctgataaatc 60
cagtgtgcag tctgatgaag tctgggtggg tgtggtctac gggctggcag ctaccatgat 120
ccaagaggta atgcactcct tttcccatct ctccaccatc tgtatcctgg ccmagaaaaa 180
```

```

cttcccttca aaccaaccaa aatttccttt caaaggcata acccaaatgc catccttggt 240
ccggtctaataaagcctccc ccatttttcc cctgggatgc attcccaggc tccctggcct 300
tncagggtct nctgtctgtg ggcatagtt tatctcctcc cacttgctgg gagctccttg 360
aaggcaaaga ctctactgcc tccatctatc cagtggaaagt ggctcttcag aggggtgcaa 420
gttagtatgt atgactgtca tctctcccaa cagggcctga cttggsaggg cttcca 476

```

<210> 329

<211> 340

<212> DNA

<213> Homo sapiens

<400> 329

```

cgagggagat tgccagcacc ctgatggaga gtgagatgat ggagatcttg tcagtgctag 60
ctaagggtga ccacagccct gtcacaaggg ctgctgcagc ctgcctggac aaagcagtgg 120
aatatgggct tatccaaccc aaccaagatg gagagtgagg gggttgtccc tgggccaag 180
gctcatgcac acgtaccta ttgtggcacg gagagtaagg acggaagcag ctttggctgg 240
tggtggctgg catgcccaat actcttgccc atcctogctt gctgccctag gatgtcctct 300
gttctgagtc agcggccacg ttcagtcaca cagccctgct 340

```

<210> 330

<211> 277

<212> DNA

<213> Homo sapiens

<400> 330

```

tgtcaccatc acattggtgc caaataccca gaagacatcg tagatgaaga gtccgcccag 60
caggatgcag ccagtgtga cattgttgag gtgcaggagc tctactccat taaggagaa 120
ggccaggcca aaaaggttgt tggcaatcca gtgcttcctc agcaggtagc agacgccaac 180
gatgtgtctc aggccaggc acaccaggtc cttgggtgtca aattcataat tgatgatctc 240
ctccttgttt tcccagaacc ctgtgtgaag agcagac 277

```

<210> 331

<211> 136

<212> DNA

<213> Homo sapiens

<400> 331

```

ttgcttccca cctcctttct ctgtcctctc ctgaggttct gccttacaat ggggacactg 60
atacaaacca cacacacaat gaggatgaaa acagataaca ggtaaaatga cctcacctgc 120
ccgggcggcc gctcga 136

```

<210> 332

<211> 184

<212> DNA

<213> Homo sapiens

<400> 332

```

ttgtgagata aacgcagata ctgcaatgca ttaaaacgct tgaaatactc atcagggatg 60
ttgctgatct tattgttgct taagtagaga gttagaagag agacaggag accagaaggc 120
agtctggcta tctgattgaa gctcaagtca aggtattcga gtgatttaag acctttaaaa 180
gcag 184

```

<210> 333

<211> 384

<212> DNA

<213> Homo sapiens

<400> 333

```
cggaaaactt cgaggaattg ctcaaagtgc tgggggtgaa tgtgatgctg aggaagattg 60
ctgtggctgc agcgtccaag ccagcagtgg agatcaaaca ggagggagac actttctaca 120
tcaaaacctc caccaccgtg cgcaccacag agattaactt caaggttggg gaggagtgtg 180
aggagcagac tgtggatggg aggccctgta agagcctggt gaaatgggag agtgagaata 240
aaatggctcg tgagcagaag ctccctgaagg gagagggccc caagacctcg tggaccagag 300
aactgaccaa cgatggggaa ctgacccctga ccatgacggc ggatgacgtt gtgtgcacca 360
gggtctacgt ccgagagtga gcgg                                     384
```

<210> 334
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 2, 165
<223> n = A,T,C or G

```
<400> 334
cnacaaacag agcagacacc ctggatccgg tcctgtctact ggccaggacg gctggaccgt 60
aaaattgaat ttccacttcc tgaccgccgc cagaagagat tgattttctc cactatcact 120
agcaagatga acctctctga ggaggttgac ttggaagact atgtngccc          169
```

<210> 335
<211> 185
<212> DNA
<213> Homo sapiens

```
<400> 335
ccaggtttgc agcccaggct gcacatcagg ggactgcctc gcaatacttc atgctgttgc 60
tgctgactga tgggtgctgtg acggatgtgg aagccacacg tgaggctgtg gtgcgtgcct 120
cgaacctgcc catgtcagtg atcattgtgg gtgtgggtgg tgctgacttt gaggccatgg 180
agcag                                     185
```

<210> 336
<211> 358
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 26
<223> n = A,T,C or G

```
<400> 336
ctgcccctgc cttacggcgg ccaganacac acccaggatg gcattggccc caaacttggg 60
tttgttctca gtcccatcca actccagcat caggttgtcc agtttctctt gctccaccac 120
agagagacct gagctgatga gggctggcgo gatggtggag ttgatgtggt ccaactgcctt 180
caggacacct ttgcctaagt aacgctgttt gtctccatcc ctgagctcca gggcctcata 240
gatgcccgtg gaggtctccac tgggcaactgc agcccggaaa agacctttgg cagtataagag 300
atccacctcc actgtggggg tcccgcggga gtccaggatc tcccgggccc agatcttc    358
```

<210> 337
<211> 271
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
 <222> 17
 <223> n = A,T,C or G

<400> 337
 cacaaagcca ccagccnngg aaatcagaat ttacttgatg caactgactt gtaatagcca 60
 gaaatcctgc ccagcatggg attcagaacc tggctctgcaa ccaaattccac cgtcaaagtt 120
 catacaggat aaaacaaatt caattgcctt ttccacatta atagcatcaa gcttccccaa 180
 caaagccaaa gttgccaccg cacaaaaaga gaatcttgtg tcaatttctc cctactttat 240
 aaaagtagat ttttcacatc ccatgaagca g 271

<210> 338
 <211> 326
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 15, 17, 18
 <223> n = A,T,C or G

<400> 338
 ctgtgctccc gactngnnca tctcaggtac caccgactgc actgggcggg gccctctggg 60
 gggaaaggct ccacggggca gggatacatc tcgaggccag tcatcctctg gaggcagccc 120
 aatcaggtca aagatthttgc ccaactggtc ggcttcagag tttccacaga agagaggctt 180
 tcgacgaaac atctctgcaa agatacagcc aacactccac atgtccacag gtgttgcata 240
 tgtggactgc agaagaactt cgggagctcg gtaccagagt gtaacaacca cgggtgtaag 300
 tgccatctgg tagctgtaga ttctgg 326

<210> 339
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 47, 54, 60, 69, 90, 91, 96, 113, 117, 119, 195
 <223> n = A,T,C or G

<400> 339
 ttcacctgag gactcatttc gtgccctttg ttgacttcaa gcaaagncct tcanggtctn 60
 caaggacgnc acatttccac ttgcgaatgn ntcanggct catcttgag aanaagnanc 120
 ccaagtgtcg gatcccagac tcgggggtaa ccttgtgggt aagagctcat ccagtttatg 180
 ctttaggacg tccanctact cgggggagct ggaagcctgc gtggatgcgg ccctgctgga 240
 cctcggccgc gaccacgcta 260

<210> 340
 <211> 220
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 15, 18
 <223> n = A,T,C or G

<400> 340
 ctggaagccc ggctngnct ggcagcggaa ggagccaggc aggttcacgc agcgggtgctg 60

```
gcagtagcgg tagcggcact cgtctatgtc cacacactcg ggcccgatct tgcggtaacc 120
atcagggcag gtgcactgat aggagccagg caagttatgg cagtccctggc tggggcgaca 180
gtcgtgcagg gcctgggcac actcgtccac atccacacag 220
```

<210> 341

<211> 384

<212> DNA

<213> Homo sapiens

<400> 341

```
ctgctaccag gggagcgaga gctgactatc ccagcctcgg ctaatgtatt ctacgccatg 60
gatggagctt cacacgattt cctcctgcgg cagcggcgaa ggtccctctac tgctacaccg 120
ggcgtcacca gtggcccgtc tgcctcagga actcctccga gtgagggagg agggggctcc 180
tttcccagga tcaaggccac agggaggaag attgcacggg cactgttctg aggaggaagc 240
cccgttggct tacagaagtc atggtgttca taccagatgt gggtagccat cctgaatggt 300
ggcaattata tcacattgag acagaaattc agaaagggag ccagccaccc tggggcagtg 360
aagtgccact ggtttaccag acag 384
```

<210> 342

<211> 245

<212> DNA

<213> Homo sapiens

<400> 342

```
ctggctaagc tcatcattgt tactgggtggg caccatgtcc ttgaagcttc aggcaagcaa 60
tgtaaccaac aagaatgacc ccaagtccat caactctcga gtcttcattg gaaacctcaa 120
cacagctctg gtgaagaaat cagatgtgga gaccatcttc tctaagtatg gccgtgtggc 180
cggctgttct gtgcacaagg gctatgcctt tgttcagtac tccaatgagc gccatgccc 240
ggcag 245
```

<210> 343

<211> 611

<212> DNA

<213> Homo sapiens

<400> 343

```
ccaaaaaaat caagatttaa tttttttatt tgcactgaaa aactaatcat aactgttaat 60
tctcagccat ctttgaagct tgaaagaaga gtctttggta ttttgtaaac gttagcagac 120
tttcctgcc a gtgcagaaa atcctattta tgaatcctgt cggtatctct tggatatctga 180
aaaaaatacc aaatagtacc atacatgagt tatttctaag ttgaaaaat aaaaagaaat 240
tgcacacac taattacaaa atacaagttc tggaaaaaat attttcttc attttaaaac 300
tttttttaac taataatggc tttgaaagaa gaggccttaat ttgggggttg taactaaaat 360
caaaagaaat gattgacttg agggctctctg tttggttaaga atacatcatt agcttaaaata 420
agcagcagaa ggtagtggg aattatgtag cttctgttaa tattaagtgt tttttgtctg 480
ttttacctca atttgaacag ataagtttgc ctgcatgctg gacatgcctc agaaccatga 540
atagcccgt a ctagatcttg ggaacatgga tcttagagtc ctttgaata agttcttata 600
taaatacccc c 611
```

<210> 344

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 1, 275, 284, 296, 297, 300

<223> n = A, T, C or G

```

<400> 344
nctcgaaaaa gcccaagaca gcagaagcag acacctccag tgaactagca aagaaaagca 60
aagaagtatt cagaaaagag atgtcccagt tcatcgcca gtgcctgaac cttaccgga 120
aacctgactg caaagtggga agaattacca caactgaaga ctttaaacad ctggctcgca 180
agctgactca cggtgttatg aataaggagc tgaagtactg taagaatcct gaggacctgg 240
agtgcaatga gaatgtgaaa cacaaaacca aggantacat taanaagtac atgcannan 300
tttggggctt g                                     311

```

```

<210> 345
<211> 201
<212> DNA
<213> Homo sapiens

```

```

<400> 345
cacacgggtca tcccgaactgc caacctggag gcccaggccc tgtggaagga gccgggcagc 60
aatgtcacca tgagtgtgga tgctgagtgt gtgcccattg tcagggacct tctcaggtac 120
ttctactccc gaaggattga catcacctg tcgtcagtca agtgcttcca caagctggcc 180
tctgcctatg gggccaggca g                                     201

```

```

<210> 346
<211> 370
<212> DNA
<213> Homo sapiens

```

```

<400> 346
ctgctccagg gcgtggtgtg ccttcgtggc ctctgcctcc tccgaggagc caggctgtgt 60
tctcttcaga atgttctgga gcagcagttt gaggcgggtg atgcgttgga agggcagaat 120
cagaaaggac ttgagggaaa ggcgctggca gacggggctg ctctccagct tctccaagac 180
ctcccggaaa ttgctgttgc tattcatcag gctctggaag gtgcgttcct gataggctctg 240
gttggtgaca taaggcaggt agaccggcg gaagtctggg gcgtggttca ggactacgtc 300
acatacttgg aaggagaaga tattgttctc aaagttctct tccaggtctg aaaggaacgt 360
ggcgctgacg                                     370

```

```

<210> 347
<211> 416
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 416
<223> n = A,T,C or G

```

```

<400> 347
ctgttgtgct gtgtatggac gtgggcttta ccatgagtaa ctccattcct ggtatagaat 60
ccccatttga acaagcaaag aaggtgataa ccatgtttgt acagcgacag gtgtttgctg 120
agaacaagga tgagattgct ttagtcctgt ttggtacaga tggcactgac aatccccctt 180
ctggtgggga tcagtatcag aacatcacag tgcacagaca tctgatgcta ccagattttg 240
atttgctgga ggacattgaa agcaaaatcc aaccaggttc tcaacaggct gacttctctg 300
atgcactaat cgtgagcatg gatgtgattc aacatgaaac aataggaaaag aagtttgag 360
aagaggcata ttgaaatatt cactgacctc aagcagcccg attcagcaaa agtcan 416

```

```

<210> 348
<211> 351
<212> DNA
<213> Homo sapiens

```

```

<400> 348

```

```

gtacaggaga ggatggcagg tgcagagcgg gcactgagct ctgcagggtga aagggtctcg 60
cagttggatg ctctcctgga ggctctgaaa ttgaaacggg caggaaatag tctggcagcc 120
tctacagcag aagaaacggc aggcagtgcc caggagacag atgccttcct 180
cttgtctcaa ctgcaaagag gcgttccttc ctctttcact aatcctcctc agcacagacc 240
ctttacgggt gtcaggctgg gggacagtaa ggtctttccc ttcccacaag gccatatctc 300
aggctgtctc agtgggggga aaccttggac aataccggg ctttcttggg c 351

```

```

<210> 349
<211> 207
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 1
<223> n = A,T,C or G

```

```

<400> 349
nccgggacat ctccaccctc aacagtggca agaagagcct ggagactgaa cacaaggcct 60
tgaccagtga gattgcactg ctgcagtcca ggctgaagac agagggctct gatctgtgcg 120
acagagtgag cgaaatgcag aagctggatg cacagggtcaa ggagctggtg ctgaagtcgg 180
cgggtggaggc tgagcgcctg gtggctg 207

```

```

<210> 350
<211> 323
<212> DNA
<213> Homo sapiens

```

```

<400> 350
ccatacaggg ctgttgccca ggccctagag gtcattcctc gtaccctgat ccagaactgt 60
ggggccagca ccatcgtct acttacctcc cttcgggcca agcacacca ggagaactgt 120
gagacctggg gtgtaaatgg tgagacgggt actttggtgg acatgaagga actgggcata 180
tgggagccat tggctgtgaa gctgcagact tataagacag cagtggagac ggcagttctg 240
ctactgcgaa ttgatgacat cgtttcaggc cacgaaaaga aaggcgatga ccagagccgg 300
caaggcgggg ctcctgatgc tgg 323

```

```

<210> 351
<211> 353
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 12, 25, 39, 42
<223> n = A,T,C or G

```

```

<400> 351
cgccgcattc cntgggtccct tccantccct tttcctttnt cngggaacgt gtatgcgggtt 60
tgtttttgtt ttgtagggtt tttttccttc tccacctctc cctgtctctt ttgtccatg 120
ttgtccgttt ctgtgggggt aggtttatgt ttttaatcat ctgaggtcac gtctatttcc 180
tocggactcg cctgcttggg ggcgattctc caccggttaa tatggtgcgt cccttttttc 240
ttttgttgcg aatctgagcc ttcttcctcc agcttctgcc ttttgaactt tgttcttcgg 300
ttctgaaacc atacttttac ctgagtttcc gtgaggctga ggctgtgtgc caa 353

```

```

<210> 352
<211> 467
<212> DNA
<213> Homo sapiens

```

<400> 352

ctgcccacac	tgatcacttg	cgagatgtcc	ttaggggtaca	agaacaggaa	ttgaagtctg	60
aatttgagca	gaacctgtct	gagaaactct	ctgaacaaga	attacaattt	cgctgtctca	120
gtcaagagca	agttgacaac	tttactctgg	atataaatac	tgctatgcc	agactcagag	180
gaatcgaaca	ggctgttcag	agccatgcag	ttgctgaaga	ggaagccaga	aaagcccacc	240
aactctggct	ttcagtggag	gcattaaagt	acagcatgaa	gacctcatct	gcagaaacac	300
ctactatccc	gctgggtagt	gcagttgagg	ccatcaaagc	caactgttct	gataatgaat	360
tcaccaagc	tttaaccgca	gctatccctc	cagagtcctt	gacccgtggg	gtgtacagtg	420
aagagaccct	tagagcccgt	ttctatgctg	ttcaaaaact	ggcccgga		467

<210> 353

<211> 350

<212> DNA

<213> Homo sapiens

<400> 353

ctgctgcagc	cacagtagtt	cctcccatgg	tgggtggccc	tcctggctct	gctggcccag	60
gaaatctgtc	cccaccagga	acagcccctg	gaaaacggcc	ccgtcctcta	ccaccttgtg	120
gaaatgctgc	acgggaactg	cctcctggag	gaccagcttt	accttcccca	gacatttgtc	180
ctgattgtgt	agttttcctg	gactgcattt	caaattgact	caggaaactgt	ttattgcatg	240
gagttacaac	aggattctga	ccatgaagtt	ctcttttagg	taacagatcc	attaactttt	300
ttgaagatgc	ttcagatcca	acaccaacaa	gggcaaacc	ctttgactgg		350

<210> 354

<211> 351

<212> DNA

<213> Homo sapiens

<400> 354

atttagatga	gatctgaggc	atggagacat	ggagacagta	tacagactcc	tagatttaag	60
tttttaggtt	tttgcttttc	taatcaccaa	ttcttatata	caatgtatat	tttagactcg	120
agcagatgat	catcttcata	ttaagtcatt	ccttttgact	gagtatggca	ggattagagg	180
gaatggcagt	atagatcaat	gtctttttct	gtaaagtata	ggaaaaacca	gagaggaaaa	240
aaagagctga	caattggaag	gtagtagaaa	attgacgata	atttcttctt	aacaaataat	300
agttgtatat	acaaggaggc	tagtcaacca	gattttattt	gttgagggcg	a	351

<210> 355

<211> 308

<212> DNA

<213> Homo sapiens

<400> 355

ttttggcgca	agttttacag	attttattaa	agtcgaagct	attggtcttg	gaagatgaaa	60
atgcaaagt	tgatgaggtg	gaattgaagc	cagatacctt	aataaaatta	tatcttggtt	120
ataaaaaata	gaaattaagg	gttaacatca	atgtgccaat	gaaaaccgaa	cagaagcagg	180
aacaagaaac	cacacacaaa	aacatcgagg	aagaccgcaa	actactgatt	caggcggcca	240
tcgtgagaat	catgaagatg	aggaagggtc	tgaaacacca	gcagttactt	ggcgaggtcc	300
tcactcag						308

<210> 356

<211> 207

<212> DNA

<213> Homo sapiens

<400> 356

ctgtcccaag	tgctcccaga	aggcaggatt	ctgaagacca	ctccagcgat	atgttcaact	60
atgaagaata	ctgcaccgcc	aacgcagtca	ctgggccttg	ccgtgcatcc	ttcccacgct	120

ggtactttga cgtggagagg aactcctgca ataacttcat ctatggaggc tgccggggca 180
ataagaacag ctaccgctct gaggagg 207

<210> 357

<211> 188

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 25, 29

<223> n = A,T,C or G

<400> 357

tcgaccacgc cctcgtagcg catgngctnc aggacgatgc tcagagtgat gaacaccccg 60
gtgcgggcca cgccagcact gcagtgcacc gtgataggcc catcctgtcc aaactgtctc 120
ttggtcttat gcacctgccc gatgaagtca atgaatccct cgctgtctt gggcacgccc 180
tgctctgg 188

<210> 358

<211> 291

<212> DNA

<213> Homo sapiens

<400> 358

ctgggagcat cggaagcta ctgccttaaa atccgatctc cccgagtgc caatttctgt 60
cccttttaag gggtcacac actaaagatt tcacatgaaa gggttgtgat tgatttgagc 120
aggcaggcgg tacgtgacag gggctgcatg caccgggtgt cagagagaaa cagaacaggg 180
cagggaattt cacaatgttc ttctatacaa tggctggaat ctatgaataa catcagtttc 240
taagttatgg gttgattttt aactactggg tttaggccag gcaggcccag g 291

<210> 359

<211> 117

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 79, 98, 100

<223> n = A,T,C or G

<400> 359

gccaccacac tccagcctgg gcaatacagc aagactgtct caaaaaaaaaa aaaaaaaaaa 60
cccaaaaaaa ctcaaaaang taatgaatga taccgaangn gccttttcta gaaaaag 117

<210> 360

<211> 394

<212> DNA

<213> Homo sapiens

<400> 360

ctgttcctct ggggtgggtc agttctagag tgggagaaaag ggagtcaggc gcattgggaa 60
tcgtgggttc agtctgggtg cagaatctgc acatttgcca agaaattttc cctgtttgga 120
aagtttgccc cagctttccc gggcacacca ccttttgtcc caagtgtctg ccggtcgacc 180
aatctgcctg ccacacattg accaagccag acccggttca ccagctcga ggatcccagg 240
ttgaagagtg cccccttgag gccctggaaa gaccaatcac tggacttctt cccttgagag 300
tcagaggtca cccgtgattc tgcctgcacc ttatcattga tctgcagtga tttctgcaaa 360
tcaagagaaa ctctgcaggg cactcccctg tttc 394

<210> 361
 <211> 394
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 28, 31
 <223> n = A,T,C or G

<400> 361
 ctgggcggat agcaccgggc atattttntt natggatgag gtctggcacc ctgagcagtc 60
 cagcgaggac ttggtcttag ttgagcaatt tggctaggag gatagtatgc agcacgggtc 120
 tgagtctgtg ggatagctgc catgaagtaa cctgaaggag gtgctggctg gtaggggttg 180
 attacagggt tgggaacagc tcgtacactt gccattctct gcatatactg gttagttagg 240
 tgagcctggc gctcttcttt gcgctgagct aaagctacat acaatggctt tgtggacctc 300
 ggccgcgacc acgctaagcc gaattccagc aactggcg cggttactag tggatccgag 360
 ctcggtacca agcttggcgt aatcatggtc atag 394

<210> 362
 <211> 268
 <212> DNA
 <213> Homo sapiens

<400> 362
 ctgcgcgtgg accagtcagc ttccgggtgt gactggagca gggcttgtcg tcttcttcag 60
 agtcactttg caggggttgg tgaagctgct cccatccatg tacagctccc agtctactga 120
 tgtttaagga tggctctcggg ggtagggccc actagaataa actgagtcca atacctctac 180
 acagttatgt ttaactgggc tctctgacac cgggaggaag gtggcggggg ttaggtgttg 240
 caaacttcaa tggttatgcg gggatgtt 268

<210> 363
 <211> 323
 <212> DNA
 <213> Homo sapiens

<400> 363
 ccttgacctt ttcagcaagt gggaagggtgt aatccgtctc cacagacaag gccaggactc 60
 gtttgtaccc gttgatgata gaatggggta ctgatgcaac agttgggtag ccaatctgca 120
 gacagacact ggcaacattg cggacaccct ccaggaagcg agaatgcaga gtttcctctg 180
 tgatatcaag cacttcaggg ttgtagatgc tgccattgtc gaacacctgc tggatgacca 240
 gcccaaagga gaagggggag atgttgagca tgttcagcag cgtggcttcg ctggctccca 300
 ctttgtctcc agtcttgatc aga 323

<210> 364
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 29
 <223> n = A,T,C or G

<400> 364
 ccaagctctc catcgtcccc gtgcgcagng gctactgggg gaacaagatc ggcaagcccc 60
 aactgtccc ttgcaagggt acaggccgct gcggctctgt gctggtacgc ctcatcactg 120

```

caccagggg cactggcatc gtctccgcac ctgtgcctaa gaagctgctc atgatggctg 180
gcatcgatga ctgctacacc tcagcccggt gctgcactgc caccctgggc aacttcgcca 240
aggccacctt tgatgccatt tctaagacct acagctacct gacccccgac ctctggaagg 300
agactgtatt caccaagtct ccctatcagg agttcactga ccacctcgtc aagaccacaca 360
ccagagtctc cgtgcagcgg actcaggctc cag                                     393

```

<210> 365

<211> 371

<212> DNA

<213> Homo sapiens

<400> 365

```

cctcctcaga gcggtagctg ttcttattgc cccggcagcc tccatagatg aagtatttgc 60
aggagttcct ctccacgtca aagtaccagc gtgggaagga tgcacggcaa ggccagtgga 120
ctgcgtttggc ggtgcagtat tcttcatagt tgaacatata gctggagtgg tcttcagaat 180
cctgccttctt gggagcactt gggacagagg aatccgctgc attcctgctg gtggacctcg 240
gccgcgacca cgctaagccg aattccagca cactggcggc cgttactagt ggatccgagc 300
tcggtaccaa gcttggcgta atcatgggtca tagctgtttc ctgtgtgaaa ttgttatccg 360
ctcacaattc c                                     371

```

<210> 366

<211> 393

<212> DNA

<213> Homo sapiens

<400> 366

```

atctcttgcc agatgggagc tctttggtga agactccttt cgggaaaagt tttttggctt 60
cttcttcagg gatggttgga aggaccatca cactatcccc atccttccaa tcaactgggg 120
tggaaccctt tttttctgct gtcagctgga gagagatgac taccctgaga atctcatcaa 180
agttcctgcc agtggttagct gggtagagga tagacagctt cagcttctta tcaggaccaa 240
aaacaaacac cacacgagct gccacaggca tgccttttcc atccttctct gctggatcca 300
gcatgcccaa caggatggca agctcccgat tcctatcatt gatgatggga aaaggtaact 360
tttctgtggg ctcttcacaa ttgtaagcat tga                                     393

```

<210> 367

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 34, 54, 55

<223> n = A,T,C or G

<400> 367

```

ccagctctgt ctcatacttg actctaaagt cttnagcagc aagacgggca ttgnnaatct 60
gcagaacgat gcgggcattg tccacagtat ttgcgaagat ctgagccctc aggtcctcga 120
tgatcttgaa gtaatggctc cagtctctga cctgggggtcc cttcttctcc aagtgtctcc 180
ggattttgtc ctccagcctc cggttctcgg tctccaggct cctcactctg tccaggtaag 240
aggccaggcg gtcgttcagg ctttgcatgg tctccttctc gttctggatg cctcccatcc 300
ctgccagacc cccggctatc ccggtgg                                     327

```

<210> 368

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 24

<223> n = A,T,C or G

<400> 368

```
ctggagaagg acttcagcag tttnaagaag tactgccaaag tcatccgtgt cattgcccac 60
accagatgc gcctgcttcc tctgcgccag aagaaggccc acctgatgga gatccagggtg 120
aacggaggca ctgtggccga gaagctggac tgggcccgcg agaggcttga gcagcaggta 180
cctgtgaacc aagtgttttg gcaggatgag atgatcgacg tcatcggggt gaccaagggc 240
aaaggctaca aaggggtcac cagtcgttgg cacaccaaga agctgccccg caagacccac 300
cgagga                                           306
```

<210> 369

<211> 394

<212> DNA

<213> Homo sapiens

<400> 369

```
tcgaccaca ccggaacacg gagagctggg ccagcattgg cacttgatag gatttcccgt 60
cggctgccac gaaagtgcgt ttctttgtgt tctcgggttg gaaccgtgat ttccacagac 120
ccttgaaata cactgcgttg acgaggacca gtctggtgag cacaccatca ataagatctg 180
gggacagcag attgtcaatc atatccctgg ttcatTTTTT aacccatgca ttgatggaat 240
cacaggcaga ggctggatcc tcaaagttca cattccggac ctacactgg aacacatctt 300
tgttccttgt aacaaaaggc acttcaattt cagaggcatt cttaacaaac acggcggttag 360
ccactgtcac aatgtcttta ttcttcttgg agac                                           394
```

<210> 370

<211> 653

<212> DNA

<213> Homo sapiens

<400> 370

```
ccaccacacc caattccttg ctggtatcat ggcagccgcc acgtgccagg attaccggct 60
acatcatcaa gtatgagaag cctgggtctc ctcccagaga agtgggtccct cgccccgcc 120
ctggtgtcac agaggctact attactggcc tggaaacggg aaccgaatat acaatttatg 180
tcattgccct gaagaataat cagaagagcg agcccctgat tggaaaggaaa aagacagacg 240
agcttcccca actggttaacc cttccacacc ccaatcttca tggaccagag atcttggatg 300
ttccttccac agttcaaaaag acccctttcg tcacccaccc tgggtatgac actggaaatg 360
gtattcagct tcctggcact tctggtcagc aaccagtggt tgggcaacaa atgatctttg 420
aggaacatgg ttttaggcgg accacaccgc ccacaacggc ccccccata aggcataagg 480
caagaccata cccgccgaat gtaggacaag aagctctctc tcagacaacc atctcatggg 540
ccccattcca ggacacttct gagtacatca ttcatgtca tcctgttggc actgatgaag 600
aacccttaca gttcagggtt cctggaactt ctaccagtgc cactctgaca gga                                           653
```

<210> 371

<211> 268

<212> DNA

<213> Homo sapiens

<400> 371

```
ctgcccagcc cccattggcg agtttgagaa ggtgtgcagc aatgacaaca agaccttca 60
ctcttctctg cacttctttg ccacaaagtg caccctggag ggcaccaaga agggccacaa 120
gctccacctg gactacatcg ggccttgcaa atacatcccc ccttgccctg actctgagct 180
gaccgaattc cccctgcgca tgcgggactg gctcaagaac gtccctgggtca ccctgtatga 240
gagggatgag gacaacaacc ttctgact                                           268
```

<210> 372

<211> 392

<212> DNA

<213> Homo sapiens

<400> 372

```

gctggtgccc ctggtgaacg tggacctcct ggattggcag gggccccagg acttagaggt 60
ggaactggtc cccctgggtc cgaaggagga aagggtgctg ctggtcctcc tgggccacct 120
ggtgctgctg gtactcctgg tctgcaagga atgcctggag aaagaggagg tcttggaagt 180
cctggtccaa agggtgacaa gggagaacca ggcggtccag gtgctgatgg tgtcccaggg 240
aaagatggcc caaggggtcc tactggtcct attggtcctc ctggcccagc tggccagcct 300
ggagataagg gtgaagggtg tgcctccgga cttccaggta tagctggacc tcgtggtagc 360
cctggtgaga gaggtgaaac ctgcggccgcg ac 392

```

<210> 373

<211> 388

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 30

<223> n = A,T,C or G

<400> 373

```

ccaagcgctc agatcggcaa ggggcaccan ttttgatctg ccagtgacac agccccacaa 60
ccaggtcagc gatgaaggta tcttcagtct ccccggaacg atgagacacc atgacgcccc 120
aaccattggc ctggggccagc ttgcacgcct gaagagactc ggacacggag ccaatctggt 180
tgactttgag caggaggcag ttgcaggact tctcgttcac ggccttggcg atcctctttg 240
ggttggtcac tgtgagatca tccccacta cctggattcc tgcactggct gtgaacttct 300
gccaagctcc ccagtcaccc tgggtcaaagg gatcttcgat agacaccact gggtagtcct 360
tgatgaagga cttgtacagg tcagccag 388

```

<210> 374

<211> 393

<212> DNA

<213> Homo sapiens

<400> 374

```

ctgacgaccg cgtgaacccc tgcatggggg gtgtcatcct cttccatgag acactctacc 60
agaaggcgga tgatgggcgt cccttcccc aagttatcaa atccaagggc ggtgttgttg 120
gcatcaaggc agacaagggc gtggtccccc tggcagggac aaatggcgag actaccaccc 180
aagggttggg tgggctgtct gagcgctgtg cccagtacaa gaaggacgga gctgacttcg 240
ccaagtggcg ttgtgtgctg aagattgggg aacacacccc ctgagccctc gccatcatgg 300
aaaatgccaa tgttctggcc cgttatgcca gtatctgcca gcagaatggc attgtgccca 360
tcgtggagcc tgagatcctc cctgatgggg acc 393

```

<210> 375

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 30, 33

<223> n = A,T,C or G

<400> 375

```

ccacaaatgg cgtgggtccat gtcataccn ttnttctgca gcctccagcc aacagacctc 60
aggaaagagg ggatgaactt gcagactctg cgcttgagat cttcaaacia gcatcagcgt 120

```

```

tttccagggc ttcccagagg tctgtgcgac tagcccctgt ctatcaaaag ttattagaga 180
ggatgaagca ttagcttgaa gcactacagg aggaatgcac cacggcagct ctccgccaat 240
ttctctcaga tttccacaga gactgtttga atgttttcaa aaccaagtat cacacttta 300
tgtacatggg ccgcaccata atgagatgtg agccttgtgc atgtggggga ggagggagag 360
agatgtactt tttaaatcat gttcccccta aaca 394

```

<210> 376

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 30

<223> n = A,T,C or G

<400> 376

```

ctgcccagcc cccattggcg agtttgattn ggtgtgcagc aatgacaaca agaccttca 60
ctcttctctg cacttctttg ccacaaagtg caccctggag ggacaccaaga agggccacaa 120
gctccacctg gactacatcg ggccttgcaa atacatcccc ccttgcttgg actctgagct 180
gaccgaattc cccctgcgca tgcgggactg gctcaagaac gtccctggta ccctgtatga 240
gagggatgag gacaacaacc ttctgactga gaagcagaag ctgcgggtga agaagatcca 300
tgagaatgag aagcgcttgg aggcaggaga ccacccctg gagctgctgg cccgggactt 360
cgagaagaac tataacatgt acatcttccc tg 392

```

<210> 377

<211> 292

<212> DNA

<213> Homo sapiens

<400> 377

```

caatgtttga tgcttaaccc cccaatttc tgtgagatgg atggccagtg caagcgtgac 60
ttgaagtgtt gcatgggcat gtgtgggaaa tcctgcgttt cccctgtgaa agcttgattc 120
ctgccatctg gaggaggctc tggagtcctg ctctgtgtgg tccaggtcct ttccaccctg 180
agacttggtc ccaccactga tatcctcctt tggggaaaagg cttggcacac agcaggcttt 240
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<210> 378

<211> 395

<212> DNA

<213> Homo sapiens

<400> 378

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agcagtatca atgtctctgc tgattgcact ggtctgaaac tcccttttga ttagctgaga 180
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ctgctggaac tgctcctcca ggagactgct gatcttggca ttctttttcc tttcatcata 360
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<210> 379

<211> 223

<212> DNA

<213> Homo sapiens

<400> 379

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ccagatgaaa tgctgccgca atggctgtgg gaaggtgtcc tgtgtcactc ccaatttctg 60

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117

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acagcttctc cctttcccaa ccaataaagt aaccactttc agc 223

<210> 380

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 30, 32

<223> n = A,T,C or G

<400> 380

tcgaccacag tattccaacc ctctgtgcn tngagaagt atggaggggtg ctgacaacca 60
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attccgcagg ggccctctc gccaaagaca gcctagagag gacggcaatg aagaagataa 180
agaaaatcaa ggagatgaga cccaagggtc gcagccacct caacgtcggg accgccgcaa 240
cttcaattac cgacgcagac gccagaaaa ccctaaacca caagatggca aagagacaaa 300
agcagccgat ccaccag 317

<210> 381

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 29, 30, 31

<223> n = A,T,C or G

<400> 381

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caagatcctg agtgacatgc gaagccaata tgaggatcat gccgagcaga accggaagga 180
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ggagcagctc cagatgagca ggtccgaggt tactgacctg cggcgcaccc ttcaggggtct 300
tgagattgag ctgcagtcac agacctcggc cgcgaccacg ctaagccgaa ttccagcaca 360
ctggcggcgc ttactagtgg atccgagctc gg 392

<210> 382

<211> 234

<212> DNA

<213> Homo sapiens

<400> 382

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ccgcgacttc gttcaggtac atgaagagct ccaaggaggt ctggtgggtg gtgccatcct 180
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<210> 383

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
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 <223> n = A,T,C or G

<400> 383
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<210> 384
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 384
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<210> 385
 <211> 2943
 <212> DNA
 <213> Homo sapiens

<400> 385
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<210> 386

<211> 2608

<212> DNA

<213> Homo sapiens

<400> 386

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<210> 387

<211> 1761

<212> DNA

<213> Homo sapiens

<400> 387

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<210> 388

<211> 772

<212> PRT

<213> Homo sapiens

<400> 388

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          20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
 35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
 50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
 65          70          75          80
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
          85          90          95
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
          100         105         110
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
          115         120         125
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
          130         135         140
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr
          145         150         155         160
His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val
          165         170         175
Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala
          180         185         190
Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn
          195         200         205
Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr
          210         215         220
Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr
          225         230         235         240
Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
          245         250         255
Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg
          260         265         270
Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu
          275         280         285
Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
          290         295         300
Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val
          305         310         315         320
Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn
          325         330         335
Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly
          340         345         350
Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser
          355         360         365
Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg
          370         375         380
Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp
          385         390         395         400
Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile
          405         410         415
Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg
          420         425         430

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Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr
    435                440                445
Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr
    450                455                460
Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His
    465                470                475                480
Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser
    485                490                495
Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val
    500                505                510
Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro
    515                520                525
Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly
    530                535                540
Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val
    545                550                555                560
Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu
    565                570                575
Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser
    580                585                590
Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu
    595                600                605
Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp
    610                615                620
Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys
    625                630                635                640
Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe
    645                650                655
Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys
    660                665                670
Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe
    675                680                685
Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr
    690                695                700
Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln
    705                710                715                720
Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile
    725                730                735
Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn
    740                745                750
Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Ala Pro His Arg Gly
    755                760                765
Gly Leu Pro Val
    770

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<210> 389

<211> 833

<212> PRT

<213> Homo sapiens

<400> 389

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Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
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Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile
    20          25          30
Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln
    35          40          45

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Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
 50          55          60
Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His
 65          70          75          80
Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr
          85          90          95
Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala
          100          105          110
Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
          115          120          125
Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr
          130          135          140
Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
          145          150          155          160
Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
          165          170          175
Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro
          180          185          190
Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu
          195          200          205
Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
          210          215          220
Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
          225          230          235          240
Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe
          245          250          255
Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser
          260          265          270
Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro
          275          280          285
Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val
          290          295          300
Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu
          305          310          315          320
Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys
          325          330          335
Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu
          340          345          350
Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn
          355          360          365
Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr
          370          375          380
Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu
          385          390          395          400
Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro
          405          410          415
Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu
          420          425          430
Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe
          435          440          445
Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala
          450          455          460
Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly
          465          470          475          480
Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
          485          490          495
His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu
          500          505          510

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[illegible]

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<210> 390
<211> 438
<212> PRT
<213> Homo sapiens
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<400> 390															
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1				5					10					15	
Leu	Gln	Tyr	Ser	Pro	Asp	Met	Gly	Lys	Gly	Ser	Ala	Thr	Phe	Asn	Ser
			20					25					30		
Thr	Glu	Gly	Val	Leu	Gln	His	Leu	Leu	Arg	Pro	Leu	Phe	Gln	Lys	Ser
		35					40					45			
Ser	Met	Gly	Pro	Phe	Tyr	Leu	Gly	Cys	Gln	Leu	Ile	Ser	Leu	Arg	Pro
50						55					60				

Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His
 65 70 75 80
 Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu
 85 90 95
 Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu
 100 105 110
 Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser
 115 120 125
 Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu
 130 135 140
 Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp
 145 150 155 160
 Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp
 165 170 175
 Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu
 180 185 190
 Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val
 195 200 205
 Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu
 210 215 220
 Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser
 225 230 235 240
 Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu
 245 250 255
 Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro
 260 265 270
 Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu
 275 280 285
 Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys
 290 295 300
 Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val
 305 310 315 320
 Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val
 325 330 335
 Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu
 340 345 350
 Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe
 355 360 365
 Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp
 370 375 380
 Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys
 385 390 395 400
 Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly
 405 410 415
 Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu
 420 425 430
 Asp Leu Glu Asp Leu Gln
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<210> 391

<211> 2627

<212> DNA

<213> Homo sapiens

<400> 391

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```

tagcatcatc attattctgg ctggagcaat tgcactcatc attggctttg gtatttcagg 180
gagacactcc atcacagtca ctactgtcgc ctacagctggg aacattgggg aggatggaat 240
cctgagctgc acttttgaac ctgacatcaa actttctgat atcgtgatac aatggctgaa 300
ggaaggtggt ttaggcttgg tccatgagtt caaagaaggc aaagatgagc tgtcggagca 360
ggatgaaatg ttcagaggcc ggacagcagt gtttctgat caagtgatag ttggcaatgc 420
ctctttgcgg ctgaaaaacg tgcaactcac agatgctggc acctacaaat gttatatcat 480
cacttctaaa ggcaagggga atgctaacct tgagtataaaa actggagcct tcagcatgcc 540
ggaagtgaat gtggactata atgccagctc agagaccttg cgggtgtgagg ctccccgatg 600
gttccccag cccacagtggt tctgggcac ccaagttgac cagggagcca acttctcgga 660
agtctccaat accagctttg agctgaactc tgagaatgtg accatgaagg ttgtgtctgt 720
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tgtcaactgt gtcaggacta agaaacctg gttttgagta gaaaagggcc tggaaagagg 2040
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ggagccacgg tgactgtatt acatgttgtt atagaaaact gatttttagag ttctgatcgt 2580
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<210> 392

<211> 309

<212> PRT

<213> Homo sapiens

<400> 392

```

His Ala Ser Ala His Ala Ser Gly Arg Gln Arg Gln Leu His Ser Ala
 1             5             10             15
Ser Thr Gln Ile Arg Trp Glu Pro Ser Pro Ala Met Ala Ser Leu Gly
 20             25             30
Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile Ile Leu Ala Gly
 35             40             45
Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser Gly Arg His Ser Ile
 50             55             60
Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile Gly Glu Asp Gly Ile

```

```

65          70          75          80
Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile Val Ile
      85          90          95
Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val His Glu Phe Lys Glu
      100         105         110
Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr
      115         120         125
Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu
      130         135         140
Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile
      145         150         155
Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala
      165         170         175
Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr
      180         185         190
Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp
      195         200         205
Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr
      210         215         220
Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val
      225         230         235
Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn
      245         250         255
Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val Thr Glu Ser Glu Ile
      260         265         270
Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser Lys Ala Ser Leu Cys
      275         280         285
Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu Leu Pro Leu Ser Pro
      290         295         300
Tyr Leu Met Leu Lys
305

```

<210> 393

<211> 282

<212> PRT

<213> Homo sapiens

<400> 393

```

Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
1      5      10      15
Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
20     25     30
Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
35     40     45
Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
50     55     60
Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
65     70     75     80
His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
85     90     95
Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
100    105    110
Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
115    120    125
Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
130    135    140
Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn

```

128

```

145          150          155          160
Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
          165          170          175
Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
          180          185          190
Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
          195          200          205
Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
          210          215          220
Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
225          230          235          240
Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
          245          250          255
Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu
          260          265          270
Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
          275          280

```

```

<210> 394
<211> 20
<212> PRT
<213> Homo sapiens

```

```

<400> 394
Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
 1          5          10          15
Ile Ile Leu Ala
          20

```

```

<210> 395
<211> 20
<212> PRT
<213> Homo sapiens

```

```

<400> 395
Ile Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile
 1          5          10          15
Ser Gly Arg His
          20

```

```

<210> 396
<211> 20
<212> PRT
<213> Homo sapiens

```

```

<400> 396
Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly
 1          5          10          15
Asn Ile Gly Glu
          20

```

```

<210> 397
<211> 20
<212> PRT

```

<213> Homo sapiens

<400> 397

Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp
1 5 10 15
Ile Lys Leu Ser
20

<210> 398

<211> 20

<212> PRT

<213> Homo sapiens

<400> 398

Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val
1 5 10 15
Leu Gly Leu Val
20

<210> 399

<211> 20

<212> PRT

<213> Homo sapiens

<400> 399

Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser
1 5 10 15
Glu Gln Asp Glu
20

<210> 400

<211> 20

<212> PRT

<213> Homo sapiens

<400> 400

Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala Asp
1 5 10 15
Gln Val Ile Val
20

<210> 401

<211> 20

<212> PRT

<213> Homo sapiens

<400> 401

Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val Gln
1 5 10 15
Leu Thr Asp Ala
20

<210> 402

<211> 21
<212> PRT
<213> Homo sapiens

<400> 402
Val Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser
1 5 10 15
Lys Gly Lys Gly Asn
20

<210> 403
<211> 20
<212> PRT
<213> Homo sapiens

<400> 403
Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe Ser
1 5 10 15
Met Pro Glu Val
20

<210> 404
<211> 20
<212> PRT
<213> Homo sapiens

<400> 404
Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr Leu
1 5 10 15
Arg Cys Glu Ala
20

<210> 405
<211> 20
<212> PRT
<213> Homo sapiens

<400> 405
Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp
1 5 10 15
Ala Ser Gln Val
20

<210> 406
<211> 20
<212> PRT
<213> Homo sapiens

<400> 406
Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn
1 5 10 15
Thr Ser Phe Glu
20

<210> 407
<211> 20
<212> PRT
<213> Homo sapiens

<400> 407
Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys Val Val
1 5 10 15
Ser Val Leu Tyr
20

<210> 408
<211> 20
<212> PRT
<213> Homo sapiens

<400> 408
Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys Met
1 5 10 15
Ile Glu Asn Asp
20

<210> 409
<211> 20
<212> PRT
<213> Homo sapiens

<400> 409
Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val Thr
1 5 10 15
Glu Ser Glu Ile
20

<210> 410
<211> 20
<212> PRT
<213> Homo sapiens

<400> 410
Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
1 5 10 15
Lys Ala Ser Leu
20

<210> 411
<211> 20
<212> PRT
<213> Homo sapiens

<400> 411
Ser Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala
1 5 10 15
Leu Leu Pro Leu

20

<210> 412

<211> 20

<212> PRT

<213> Homo sapiens

<400> 412

```

Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu Leu Pro Leu Ser Pro Tyr
 1             5             10             15
Leu Met Leu Lys
                20

```

<210> 413

<211> 35

<212> PRT

<213> Homo sapiens

<400> 413

```

Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly
 1             5             10             15
Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile
                20             25             30
Lys Leu Ser
                35

```

<210> 414

<211> 35

<212> PRT

<213> Homo sapiens

<400> 414

```

Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser
 1             5             10             15
Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln
                20             25             30
Val Ile Val
                35

```

<210> 415

<211> 65

<212> PRT

<213> Homo sapiens

<400> 415

```

Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe Ser
 1             5             10             15
Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr Leu Arg
                20             25             30
Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp Ala Ser
                35             40             45
Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr Ser Phe
                50             55             60
Glu

```

65

<210> 416
<211> 10
<212> PRT
<213> Homo sapiens

<400> 416
Lys Leu Ser Asp Ile Val Ile Gln Trp Leu
1 5 10

<210> 417
<211> 10
<212> PRT
<213> Homo sapiens

<400> 417
Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile
1 5 10

<210> 418
<211> 10
<212> PRT
<213> Homo sapiens

<400> 418
Leu Leu Asn Ser Lys Ala Ser Leu Cys Val
1 5 10

<210> 419
<211> 10
<212> PRT
<213> Homo sapiens

<400> 419
Ser Leu Cys Val Ser Ser Phe Phe Ala Ile
1 5 10

<210> 420
<211> 10
<212> PRT
<213> Homo sapiens

<400> 420
Val Leu Tyr Asn Val Thr Ile Asn Asn Thr
1 5 10

<210> 421
<211> 10
<212> PRT
<213> Homo sapiens

134

<400> 421
Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
1 5 10

<210> 422
<211> 10
<212> PRT
<213> Homo sapiens

<400> 422
Leu Leu Pro Leu Ser Pro Tyr Leu Met Leu
1 5 10

<210> 423
<211> 10
<212> PRT
<213> Homo sapiens

<400> 423
Cys Met Ile Glu Asn Asp Ile Ala Lys Ala
1 5 10

<210> 424
<211> 10
<212> PRT
<213> Homo sapiens

<400> 424
Lys Thr Gly Ala Phe Ser Met Pro Glu Val
1 5 10

<210> 425
<211> 10
<212> PRT
<213> Homo sapiens

<400> 425
Trp Ala Leu Leu Pro Leu Ser Pro Tyr Leu
1 5 10

<210> 426
<211> 10
<212> PRT
<213> Homo sapiens

<400> 426
Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile
1 5 10

<210> 427
<211> 10
<212> PRT

<213> Homo sapiens

<400> 427

Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys
1 5 10

<210> 428

<211> 10

<212> PRT

<213> Homo sapiens

<400> 428

Ala Leu Leu Pro Leu Ser Pro Tyr Leu Met
1 5 10

<210> 429

<211> 10

<212> PRT

<213> Homo sapiens

<400> 429

Gln Leu Leu Asn Ser Lys Ala Ser Leu Cys
1 5 10

<210> 430

<211> 10

<212> PRT

<213> Homo sapiens

<400> 430

Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile
1 5 10

<210> 431

<211> 10

<212> PRT

<213> Homo sapiens

<400> 431

Trp Leu Lys Glu Gly Val Leu Gly Leu Val
1 5 10

<210> 432

<211> 10

<212> PRT

<213> Homo sapiens

<400> 432

Leu Gln Leu Leu Asn Ser Lys Ala Ser Leu
1 5 10

<210> 433

<211> 10
<212> PRT
<213> Homo sapiens

<400> 433
Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile
1 5 10

<210> 434
<211> 10
<212> PRT
<213> Homo sapiens

<400> 434
Gly Ile Ser Gly Arg His Ser Ile Thr Val
1 5 10

<210> 435
<211> 10
<212> PRT
<213> Homo sapiens

<400> 435
Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile
1 5 10

<210> 436
<211> 9
<212> PRT
<213> Homo sapiens

<400> 436
Ala Leu Leu Pro Leu Ser Pro Tyr Leu
1 5

<210> 437
<211> 9
<212> PRT
<213> Homo sapiens

<400> 437
Ser Leu Cys Val Ser Ser Phe Phe Ala
1 5

<210> 438
<211> 9
<212> PRT
<213> Homo sapiens

<400> 438
Ile Leu Phe Trp Ser Ile Ile Ser Ile
1 5

<210> 439

<211> 9

<212> PRT

<213> Homo sapiens

<400> 439

Gln Leu Leu Asn Ser Lys Ala Ser Leu
1 5

<210> 440

<211> 9

<212> PRT

<213> Homo sapiens

<400> 440

Lys Val Val Ser Val Leu Tyr Asn Val
1 5

<210> 441

<211> 9

<212> PRT

<213> Homo sapiens

<400> 441

Ile Leu Ala Gly Ala Ile Ala Leu Ile
1 5

<210> 442

<211> 9

<212> PRT

<213> Homo sapiens

<400> 442

Trp Leu Lys Glu Gly Val Leu Gly Leu
1 5

<210> 443

<211> 9

<212> PRT

<213> Homo sapiens

<400> 443

Ile Ile Leu Ala Gly Ala Ile Ala Leu
1 5

<210> 444

<211> 9

<212> PRT

<213> Homo sapiens

<400> 444

Asn Val Thr Met Lys Val Val Ser Val

1 5

<210> 445
<211> 9
<212> PRT
<213> Homo sapiens

<400> 445
Glu Met Phe Arg Gly Arg Thr Ala Val
1 5

<210> 446
<211> 9
<212> PRT
<213> Homo sapiens

<400> 446
Ala Val Phe Ala Asp Gln Val Ile Val
1 5

<210> 447
<211> 9
<212> PRT
<213> Homo sapiens

<400> 447
Leu Leu Pro Leu Ser Pro Tyr Leu Met
1 5

<210> 448
<211> 9
<212> PRT
<213> Homo sapiens

<400> 448
Leu Leu Asn Ser Lys Ala Ser Leu Cys
1 5

<210> 449
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<400> 458

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Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
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Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
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Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys
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<212> PRT

<213> Homo sapiens

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His	Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	
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Tyr	His	Leu	Lys	Thr	Leu	Thr	Leu	Asn	Phe	Thr	Ile	Ser	Asn	Leu	Gln
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Pro	Val	Gly	Pro	Gly	Leu	Asp	Ile	Gln	Gln	Leu	Tyr	Trp	Glu	Leu	Ser
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Asn	Leu	Val	Pro	Arg	Leu	Pro	Ala	Leu	Ser	Trp	Cys	Tyr	Ser	Leu	Ser
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Thr	Ser	Pro	Ser	Pro	Thr	Cys	Gly	Met	Arg	Arg	Thr	Cys	Ser	Thr	Leu
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<212> PRT
<213> Homo sapiens
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<211> 2996
<212> DNA
<213> Homo sapiens
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<210> 463

<211> 3557

<212> DNA

<213> Homo sapiens

<400> 463

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<210> 464

<211> 2712

<212> DNA

<213> Homo sapiens

<400> 464

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<210> 465

<211> 1175

<212> DNA

<213> Homo sapiens

<400> 465

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ggacagtctc tatgtcaatg gtttcaccca tcggagctct gtaccacca ccagcaccg 600
ggtggtcagc gaggagccat tcacactgaa cttcaccatc aacaacctgc gctacatggc 660
ggacatgggc caaccggct ccctcaagtt caacatcac gacaacgtca tgaagcacct 720

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gctcagtcct ttgttccaga ggagcagcct ggggtgcacgg tacacaggct gcaggggtcat 780
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<210> 466

<211> 1959

<212> DNA

<213> Homo sapiens

<400> 466

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```

<210> 467

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 467

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cccaagccag ccaccacatt cctgcctcct ctgtcagaag ccacaacagc catgggggtac 240
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cctgagaagg atggggcgagc cactggtgtg gacaccacct gcacctacca cctgaccct 480
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<210> 468

<211> 231

<212> DNA

<213> Homo sapiens

<400> 468

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taccatattc ccaggacaaa gccagccag gcaccaccaa ttaccagagg aacaaaagga 180
atattgagga tgcgctcaac caactcttcc gaaacagcag catcgagagt t 231

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<210> 469

<211> 607

<212> DNA

<213> Homo sapiens

<400> 469

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agggtcaggt ggtgtccaca ccagtggctg ccccatcctt ctcaggccag gtgctgaagg 180
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ccaggttcat tgtaaccgtt aaggtagagg ctgtctttgt ccagagagta gggggccagc 420
cgggtgatgc catgggtctg ctggctcagc tcatggaaca cctgcttgat aggcagacct 480
gggccgctga ggggtgcag gtaggtgcag aggaggtcca ccggtgtctc agcaccgttc 540
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```

<210> 470

<211> 981

<212> DNA

<213> Homo sapiens

<400> 470

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ggacaattcc caacttttcc c 981

```

<210> 471

<211> 959

<212> DNA

<213> Homo sapiens

<400> 471

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aggaccctct ctgtagtggt gaacttcctg gagccaggcc acatgttctc ctcataccgc 180
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<210> 472

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 472

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gtcaatggtt tcacccatcg gacctctgtg cccaccaeca gcactcctgg gacctccaca 180
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catcgccctg gctccaggaa gttcaacacc actgagaggg tcctgcagac tctgcttggg 360
cctatgttca agaacaccag tgttggcctt ctgtactctg gctgcagact gaccttgctc 420
aggtccgaga aggatggagc agccactgga gtggatgcca tctgcacca ccgtcttgac 480

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```

cccaaaagcc ctggagtgga cagggagcag ctatactggg agctgagcca gctgaccaat 540
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accatttga tccctgtgcc caccagcagc actcctggga cctccacagt ggaccttggg 660
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<210> 473

<211> 689

<212> DNA

<213> Homo sapiens

<400> 473

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<210> 474

<211> 495

<212> DNA

<213> Homo sapiens

<400> 474

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aggatcaatgc taccctggtg caatgaaccg agtttcatgg tacagggaca attgaagatt 180
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agatttcaac cacatcacag ccactacca ttgacataga gactgttcct gtccagggtg 420
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<210> 475

<211> 192

<212> DNA

<213> Homo sapiens

<400> 475

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agtggccagg ctactaccag tcacacctag acctggagga tctgcaatga ctggaacttg 60
ccggtgcttg gggatagcct ctcatcaat ggctatgcac ccagaattt atcaatccgg 120

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ggcgagtacc agataaattt ccacattgtc aactggaacc tcagtaatcc agaccccaca 180
tcctcagagt ac 192

<210> 476

<211> 500

<212> DNA

<213> Homo sapiens

<400> 476

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<210> 477

<211> 191

<212> DNA

<213> Homo sapiens

<400> 477

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agaagtaggc ctttttgaaa tatataaagt tctccacttt tgaacatggt gtttctttcc 180
cacctccacg a 191

<210> 478

<211> 914

<212> PRT

<213> Homo sapiens

<400> 478

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Asn	Leu	Val	Pro	Arg	Leu	Pro	Ala	Leu	Ser	Trp	Cys	Tyr	Ser	Leu	Ser	35	40	45	
Thr	Ser	Pro	Ser	Pro	Thr	Cys	Gly	Met	Arg	Arg	Thr	Cys	Ser	Thr	Leu	50	55	60	
Ala	Pro	Gly	Ser	Ser	Thr	Pro	Arg	Arg	Gly	Ser	Phe	Arg	Ala	Trp	Ser	65	70	75	
Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	85	90	95	
Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Thr	Ala	Thr	Gly	Val	Asp	Ala	100	105	110	
Ile	Cys	Thr	His	His	Pro	Asp	Pro	Lys	Ser	Pro	Arg	Leu	Asp	Arg	Glu	115	120	125	
Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Asn	Ile	Thr	Glu	Leu	130	135	140	
Gly	Pro	Tyr	Ala	Leu	Asp	Asn	Asp	Ser	Leu	Phe	Val	Asn	Gly	Phe	Thr	145	150	155	
His	Arg	Ser	Ser	Val	Ser	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Val	165	170	175	

Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala
 180 185 190
 Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn
 195 200 205
 Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr
 210 215 220
 Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr
 225 230 235 240
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
 245 250 255
 Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg
 260 265 270
 Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu
 275 280 285
 Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
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 Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val
 305 310 315 320
 Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn
 325 330 335
 Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly
 340 345 350
 Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser
 355 360 365
 Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg
 370 375 380
 Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp
 385 390 395 400
 Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile
 405 410 415
 Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg
 420 425 430
 Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr
 435 440 445
 Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr
 450 455 460
 Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His
 465 470 475 480
 Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser
 485 490 495
 Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val
 500 505 510
 Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro
 515 520 525
 Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly
 530 535 540
 Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val
 545 550 555 560
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu
 565 570 575
 Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser
 580 585 590
 Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu
 595 600 605
 Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp
 610 615 620
 Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys
 625 630 635 640

Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe
 645 650 655
 Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys
 660 665 670
 Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe
 675 680 685
 Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr
 690 695 700
 Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln
 705 710 715 720
 Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile
 725 730 735
 Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn
 740 745 750
 Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe
 755 760 765
 Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr
 770 775 780
 Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys
 785 790 795 800
 Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu
 805 810 815
 Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr
 820 825 830
 Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn
 835 840 845
 Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu
 850 855 860
 Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly
 865 870 875 880
 Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val
 885 890 895
 Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp
 900 905 910
 Leu Gln

<210> 479

<211> 1148

<212> PRT

<213> Homo sapiens

<400> 479

Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
 1 5 10 15
 Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 20 25 30
 Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
 35 40 45
 Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
 50 55 60
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
 65 70 75 80
 Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
 85 90 95
 Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
 100 105 110

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Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile
    115                120                125
Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
    130                135                140
Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
    145                150                155                160
Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
    165                170                175
Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys
    180                185                190
Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
    195                200                205
Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
    210                215                220
Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg
    225                230                235                240
Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu
    245                250                255
Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser
    260                265                270
Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg
    275                280                285
Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
    290                295                300
Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser
    305                310                315                320
Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
    325                330                335
Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro
    340                345                350
Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
    355                360                365
Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly His Tyr Ala Leu Asp
    370                375                380
Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser
    385                390                395                400
Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys
    405                410                415
Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile
    420                425                430
Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
    435                440                445
Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
    450                455                460
Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
    465                470                475                480
Ser Gly Ser Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala
    485                490                495
Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly Pro
    500                505                510
Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr His
    515                520                525
Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
    530                535                540
Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly
    545                550                555                560
Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu
    565                570                575

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Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile
 580 585 590
 Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser
 595 600 605
 Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser
 610 615 620
 Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu
 625 630 635 640
 Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu
 645 650 655
 Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu
 660 665 670
 Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Leu Asp
 675 680 685
 Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu
 690 695 700
 Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu
 705 710 715 720
 Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly
 725 730 735
 Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg
 740 745 750
 Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln
 755 760 765
 Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
 770 775 780
 Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile
 785 790 795 800
 Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln
 805 810 815
 Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr
 820 825 830
 Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His
 835 840 845
 Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr
 850 855 860
 Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
 865 870 875 880
 Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
 885 890 895
 Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
 900 905 910
 Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
 915 920 925
 Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
 930 935 940
 Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser
 945 950 955 960
 Thr Gln His Phe Tyr Pro Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser
 965 970 975
 Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
 980 985 990
 Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
 995 1000 1005
 Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn
 1010 1015 1020
 Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala
 1025 1030 1035 1040

161

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Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr
      1045      1050      1055
Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val
      1060      1065      1070
Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn
      1075      1080      1085
Ser Asp Leu Pro Phe Trp Ala Val Ile Phe Ile Gly Leu Ala Gly Leu
      1090      1095      1100
Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg
      1105      1110      1115      1120
Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly
      1125      1130      1135
Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
      1140      1145

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<210> 480

<211> 230

<212> PRT

<213> Homo sapiens

<400> 480

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Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
  1      5      10      15
Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
      20      25      30
Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala
      35      40      45
Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
      50      55      60
Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
      65      70      75      80
Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
      85      90      95
Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr
      100      105      110
Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu
      115      120      125
Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
      130      135      140
Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly
      145      150      155      160
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly
      165      170      175
Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
      180      185      190
Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
      195      200      205
Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Leu Glu Trp Thr Gly
      210      215      220
Ser Ser Tyr Thr Gly Ser
      225      230

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<210> 481

<211> 210

<212> PRT

<213> Homo sapiens

<400> 481

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Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 1          5          10          15
Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
      20          25          30
Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr
      35          40          45
Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser
      50          55          60
Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
      65          70          75          80
His Asn Ile Thr Glu Leu Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu
      85          90          95
Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr
      100          105          110
Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser
      115          120          125
Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu
      130          135          140
Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly
      145          150          155          160
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg
      165          170          175
Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
      180          185          190
Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp
      195          200          205
Ala Ile
      210

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<210> 482

<211> 97

<212> PRT

<213> Homo sapiens

<400> 482

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Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
 1          5          10          15
Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
      20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
      35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
      50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Cys Ser
      65          70          75          80
Gly Pro Cys Ser Arg Ala Pro Val Leu Ala Leu Cys Thr Leu Ala Ala
      85          90          95
Asp

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<210> 483

<211> 438

<212> PRT

<213> Homo sapiens

<400> 483

```

Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn
 1      5      10      15
Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser
 20      25      30
Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser
 35      40      45
Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro
 50      55      60
Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His
 65      70      75      80
Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu
 85      90      95
Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu
100      105      110
Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser
115      120      125
Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu
130      135      140
Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp
145      150      155      160
Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp
165      170      175
Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu
180      185      190
Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val
195      200      205
Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu
210      215      220
Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser
225      230      235      240
Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu
245      250      255
Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro
260      265      270
Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu
275      280      285
Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys
290      295      300
Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val
305      310      315      320
Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val
325      330      335
Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu
340      345      350
Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser
355      360      365
Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp
370      375      380
Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys
385      390      395      400
Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly
405      410      415
Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu
420      425      430
Asp Leu Glu Asp Leu Gln
435

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<210> 484
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Thr Leu Lys Ser Trp Ala Pro Thr Pro Trp Thr Gly Thr Val Ser
 1 5 10 15
 Met Ser Met Val Ser Pro Ile Arg Ala Leu Cys Pro Pro Ala Leu
 20 25 30
 Leu Gly Pro Pro Gln Trp Ile Ser Glu Pro Gln Trp Thr Pro Ser Ser
 35 40 45
 Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe
 50 55 60
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly
 65 70 75 80
 His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 85 90 95
 Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser
 100 105 110
 Gly Cys Arg Leu Thr Ser Leu Arg Ser Lys Lys Asp Gly Ala Ala Thr
 115 120 125
 Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly
 130 135 140
 Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly
 145 150 155 160
 Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val
 165 170 175
 Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser Thr Pro Gly
 180 185 190
 Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Leu Pro
 195 200 205
 Ala Thr Gln Ser Leu Ala Leu Ser
 210 215

<210> 485
 <211> 268
 <212> PRT
 <213> Homo sapiens

<400> 485
 Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr
 1 5 10 15
 Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu
 20 25 30
 Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu
 35 40 45
 Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser
 50 55 60
 Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
 65 70 75 80
 Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp
 85 90 95
 Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro
 100 105 110

165

Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys
 115 120 125
 Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn
 130 135 140
 Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr
 145 150 155 160
 Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Val Asp Ser
 165 170 175
 Ile Leu Pro Leu Gln Pro His Asn Tyr Gly Cys Trp Pro Ser Pro Gly
 180 185 190
 Thr Ile His Pro Gln Leu His His Gln Pro Ala Val Trp Gly Gly
 195 200 205
 His Gly Ser Pro Trp Leu Gln Glu Val Gln His His Arg Glu Gly Pro
 210 215 220
 Ala Gly Ser Ala Trp Ser His Ile Gln Glu His Gln Cys Trp Pro Ser
 225 230 235 240
 Val Leu Trp Leu Gln Thr Asp Leu Ser Gln Val Gln Glu Gly Trp Ser
 245 250 255
 Ser His Trp Ser Gly Cys His Leu His Pro Ser Ser
 260 265

<210> 486

<211> 304

<212> PRT

<213> Homo sapiens

<400> 486

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 1 5 10 15
 Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 20 25 30
 Tyr Ser Gly Cys Arg Leu Thr Leu Arg Pro Glu Lys Asp Gly Glu
 35 40 45
 Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly
 50 55 60
 Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr
 65 70 75 80
 His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
 85 90 95
 Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr
 100 105 110
 Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn
 115 120 125
 Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn
 130 135 140
 Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg
 145 150 155 160
 Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg
 165 170 175
 Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr
 180 185 190
 Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His
 195 200 205
 Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser
 210 215 220
 Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Pro
 225 230 235 240

Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro
 245 250 255
 Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr
 260 265 270
 Leu Asn Ser His Leu Gln Ser Pro Val Phe Thr Arg Tyr Gly Gln Gly
 275 280 285
 Leu Lys Val His Ser Ile His Arg Gly Gly Ser Phe Ser Asn Trp Ser
 290 295 300

<210> 487

<211> 294

<212> PRT

<213> Homo sapiens

<400> 487

Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn
 1 5 10 15
 Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr
 20 25 30
 Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro
 35 40 45
 Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe
 50 55 60
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His
 65 70 75 80
 Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly
 85 90 95
 Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser
 100 105 110
 Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr
 115 120 125
 Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly
 130 135 140
 Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn
 145 150 155 160
 Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val
 165 170 175
 Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly
 180 185 190
 Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro
 195 200 205
 Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe
 210 215 220
 Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser
 225 230 235 240
 Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser Pro
 245 250 255
 Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
 260 265 270
 Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala
 275 280 285
 Val Cys Leu Tyr Arg Pro
 290

<210> 488

<211> 233

<212> PRT

<213> Homo sapiens

<400> 488

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Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe
 1           5           10          15
His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu
          20          25          30
Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His
          35          40          45
Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys
          50          55          60
Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
65          70          75          80
Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe
          85          90          95
Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His
          100         105         110
Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val
          115         120         125
Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly
          130         135         140
Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp
145         150         155         160
Gly Tyr Phe Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu
          165         170         175
Pro Phe Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu
          180         185         190
Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys
          195         200         205
Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln
210         215         220
Ser His Leu Asp Leu Glu Asp Leu Gln
225         230

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<210> 489

<211> 178

<212> PRT

<213> Homo sapiens

<400> 489

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Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe
 1           5           10          15
His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu
          20          25          30
Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His
          35          40          45
Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys
          50          55          60
Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
65          70          75          80
Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe
          85          90          95
Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His
          100         105         110
Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val
          115         120         125

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168

Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly
 130 135 140
 Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp
 145 150 155 160
 Gly Tyr Phe Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu
 165 170 175
 Pro Phe

<210> 490
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 490
 Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu Ala Pro Gly Ser
 1 5 10 15

<210> 491
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 491
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<400> 493
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<210> 494
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<400> 494
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<210> 495
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1 5 10 15

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<400> 498
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1 5 10 15

<210> 499
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<213> Homo sapiens

<400> 499
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<400> 500

170

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<210> 501

<211> 15

<212> PRT

<213> Homo sapiens

<400> 501

Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr
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<210> 502

<211> 15

<212> PRT

<213> Homo sapiens

<400> 502

Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg
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<210> 503

<211> 15

<212> PRT

<213> Homo sapiens

<400> 503

Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly
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<210> 504

<211> 15

<212> PRT

<213> Homo sapiens

<400> 504

Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp
1 5 10 15

<210> 505

<211> 15

<212> PRT

<213> Homo sapiens

<400> 505

Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln
1 5 10 15

<210> 506

<211> 15

<212> PRT

<213> Homo sapiens

<400> 506

Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
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<210> 507

<211> 15

<212> PRT

<213> Homo sapiens

<400> 507

His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser
1 5 10 15

<210> 508

<211> 15

<212> PRT

<213> Homo sapiens

<400> 508

Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln
1 5 10 15

<210> 509

<211> 15

<212> PRT

<213> Homo sapiens

<400> 509

Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser
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<210> 510

<211> 15

<212> PRT

<213> Homo sapiens

<400> 510

Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu
1 5 10 15

<210> 511

<211> 15

<212> PRT

<213> Homo sapiens

<400> 511

Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
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<210> 512

<211> 450

<212> DNA

<213> Homo sapiens

<400> 512

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acttcaccat ctccaatctc cagtattcac cagatatggg caagggctca gctacattca 180
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ctggtgtgga caccacctgc acctaccacc ctgaccctgt gggccccggg ctggacatac 360
agcagcttta ctgggagctg agtcagctga cccatggtgt cacccaactg ggcttctatg 420
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<210> 513

<211> 402

<212> DNA

<213> Homo sapiens

<400> 513

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ccctcaagtt caacatcaca gacaacgtca tgaagcacct gctcagtcct ttgttccaga 180
ggagcagcct ggggtgcacgg tacacaggct gcagggtcat cgcactaagg tctgtgaaga 240
acgggtgctga gacacgggtg gacctcctct gcacctacct gcagcccctc agcggcccag 300
gtctgcctat caagcagggtg ttccatgagc tgagccagca gacctatggc atcacccggc 360
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<210> 514

<211> 465

<212> DNA

<213> Homo sapiens

<400> 514

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tactattcac cctcaacttc accatcacta acctgcggta tgaggagaac atgtggcctg 180
gctccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg ccctgtttca 240
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aagatgggga agccaccgga gtggatgcc a tctgcaccca ccgccctgac cccacaggcc 360
ctgggctgga cagagagcag ctgtatttgg agctgagcca gctgacccac agcatcactg 420
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<210> 515

<211> 463

<212> DNA

<213> Homo sapiens

<400> 515

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tgctattcac tctcaacttc accatcacca acctgcggta tgaggagaac atgcagcacc 180
ctggctccag gaagttcaac accacggaga gggctccttca gggcctgggc cctgttcaag 240
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gatgggacag ccactggagt ggatgccatc tgcacccacc accctgaccc caaaagccct 360
aggctggaca gagagcagct gtattgggag ctgagccagc tgacccacaa tatcactgag 420
ctggggcccct atgccctgga caacgacagc ctctttgtca atg                               463

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<210> 516

<211> 156

<212> DNA

<213> Homo sapiens

<400> 516

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acagagagca gctgtatttg gagctgagcc agctgaccca cagcatcact gagctggggc 120
cctacaccct ggacagggac agtctctatg tcaatg 156
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<210> 517

<211> 450

<212> DNA

<213> Homo sapiens

<400> 517

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gttacaatga acctggtcta gatgagcctc ctacaactcc caagccagcc accacattcc 60
tgcctcctct gtcagaagcc acaacagcca tggggtacca cctgaagacc ctacactca 120
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actccaccga gggggtcctt cagcacctgc tcagaccctt gttccagaag agcagcatgg 240
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ctggtgtgga caccacctgc acctaccacc ctgaccctgt gggcccggg ctggacatac 360
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<210> 518

<211> 402

<212> DNA

<213> Homo sapiens

<400> 518

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ccctcaagtt caacatcaca gacaacgtca tgaagcacct gctcagtcct ttgttccaga 180
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gtctgcctat caagcaggtg ttccatgagc tgagccagca gacctatggc atcaccgggc 360
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<210> 519

<211> 465

<212> DNA

<213> Homo sapiens

<400> 519

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tactattcac cctcaacttc accatcacta acctgcggtg tgaggagaac atgtggcctg 180
gtccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg cccttggtca 240
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aagatgggga agccaccgga gtggatgcca tctgcaccca ccgccctgac cccacaggcc 360
ctgggctgga cagagagcag ctgtatttgg agctgagcca gctgaccac agcatcactg 420
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<210> 520

<211> 468

<212> DNA

<213> Homo sapiens

<400> 520

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tgctattcac tctcaacttc accatcacca acctgcggta tgaggagaac atgcagcacc 180
ctggctccag gaagttcaac accacggaga gggctcctca gggcctgctc aggtccctgt 240
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aaaaggatgg gacagccact ggagtggatg ccatctgcac ccaccaccct gacccccaaa 360
gccctaggct ggacagagag cagctgtatt gggagctgag ccagctgacc cacaatatca 420
ctgagctggg ccactatgcc ctggacaacg acagcctctt tgtcaatg 468

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<210> 521

<211> 468

<212> DNA

<213> Homo sapiens

<400> 521

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tgctattcac aattaacttc accatcacta acctgcggta tgaggagaac atgcacacc 180
ctggctctag aaagttaaacc accacggaga gagtccctca gggctctgctc aggcctgtgt 240
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agaaggatgg ggcagccacc aaagtggatg ccatctgcac ctaccgccct gatccccaaa 360
gccctggact ggacagagag cagctatact gggagctgag ccagctaacc cacagcatca 420
ctgagctggg cccctacacc ctggacaggg acagtctcta tgtcaatg 468

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<210> 522

<211> 262

<212> DNA

<213> Homo sapiens

<400> 522

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tactctggtt gcagactgac cttgtctagg cctgagaagg atggggcagc caccagagtg 120
gatgctgtct gaccccatcg tcctgacccc aaaagccctg gactggacag agagcggctg 180
tactggaagc tgagccagct gaccacggc atcactgagc tgggccccta caccctggac 240
aggcacagtc tctatgtcaa tg 262

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<210> 523

<211> 302

<212> DNA

<213> Homo sapiens

<400> 523

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tgcttgggtc cttgttcaag aactccagtg tcggccctct gtactctggc tgagactga 120
tctctctcag gtctgagaag gatggggcag ccactggagt ggatgccatc tgacccacc 180
accttaacct tcaaagcctg gactggacag ggagcagctg tactggcagc tgagccagat 240
gaccaatggc atcaaagagc tgggccccta caccctggac cggaacagtc tctacgtcaa 300
tg 302

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<210> 524

<211> 468

<212> DNA

<213> Homo sapiens

<400> 524

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tgccattcac cctaaacttc accatcacca acctgcagta tgaggaggac atgcatcgcc 180
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tcaagaactc cagtgttggc cctctgtact ctggctgcag actgacctct ctcaggcccc 300
agaaggatgg ggcagcaact ggaatggatg ctgtctgcct ctaccaccct aatcccaaaa 360
gacctgggct ggacagagag cagctgtact gggagctaag ccagctgacc cacaacatca 420
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<210> 525

<211> 470

<212> DNA

<213> Homo sapiens

<400> 525

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taccattcac attcaacttt accatcacca acctgcatta tgaggaaaac atgcaacacc 180
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agaaggatgg ggcagcaact ggaatggatg ctgtctgtct ctaccgacct taatcccatc 360
ggacctgggc tggacagaga gcagctgtac tgggagctga gccagctgac ccacgacatc 420
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<210> 526

<211> 467

<212> DNA

<213> Homo sapiens

<400> 526

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taccattcac tttcaacttt accatcacca acctgcatta tgaggaaaac atgcaacacc 180
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gaagcaggag gcagccactg gagtggacac catctgcact caccgccttg accctctaaa 360
ccctggactg gacagagagc agctatactg ggagctgagc aaactgacct gtggcatcat 420
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<210> 527

<211> 468

<212> DNA

<213> Homo sapiens

<400> 527

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tgccattcac cctcaacttc accatcacca acttgcagta tgaggaggcc atgcgacacc 180
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agaaggacaa ggcagccacc agagtggatg ccactctgtac ccaccaccct gaccctcaaa 360
gccctggact gaacagagag cagctgtact gggagctgag ccagctgacc cacggcatca 420
ctgagctggg cccctacacc ctggacaggg acagtctcta tgtcaatg 468

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<210> 528

<211> 537

<212> DNA

<213> Homo sapiens

<400> 528

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tgctattcac aattaacttc accatcacta acctgcggta tgaggagaac atgcatcacc 180
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<210> 529

<211> 231

<212> DNA

<213> Homo sapiens

<400> 529

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gcggcccagg tctgcctatc aagcagggtg tccatgagct gagccagcag acccatggca 180
tcaccgggct gggccccctac tctctggaca aagacagcct ctaccttaac g 231

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<210> 530

<211> 376

<212> DNA

<213> Homo sapiens

<400> 530

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acttcaccat ctccaatctc cagtattcac cagatatggg caagggctca gctacattca 180
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gacaccacct gcacctacca cctgaccct gtgggccccg ggctggacat acagcagctt 300
tactgggagc tgagttagct gaccatggt gtaccccaac tgggcttcta tgcctggac 360
agcgatagct cttcat 376

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<210> 531

<211> 75

<212> DNA

<213> Homo sapiens

<400> 531

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gtctctatgt caatg 75

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<210> 532

<211> 906

<212> DNA

<213> Homo sapiens

<400> 532

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tgccgttcac cctcaacttt accatcacca atctgcagta tggggaggac atgcgtcacc 180
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agaaggatgg ggcagccact ggagtggatg ccatctgcac ccaccacctt aacctcaaa 360
gccctggact ggacagggag cagctgtact ggcagctgag ccagagacca caacctcatt 420
tatcacctat tctgagacac acacaagttc agccattcca actctccctg tctccccctg 480

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gtgcatcaaa gatgctgacc tcaactggta tcagttctgg gacagacagc actacaactt 540
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ctgcagagac caacacaatg gttcccagga caactcccaa gttttcccat agtaagtcag 660
acaccacact cccagtagcc atcaccagtc ctgggcccaga agccagttca gctgtttcaa 720
cgacaactat ctcaacctgat atgtcagatc tgggtgacctc actgggtccct agttctggga 780
cagacaccag tacaaccttc ccaacattga gtgagacccc atatgaacca gagactacag 840
ccacgtggct cactcatcct gcagaaacca gaacaacggg ttctgggaca attcccaact 900
tttccc
906

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<210> 533

<211> 404

<212> DNA

<213> Homo sapiens

<400> 533

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tgccgttcac cctcaacttt accatcacca atctgcagta tggggaggac atgcgtcacc 180
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tcaagaactc cagtgtcggc cctctgtact ctggctgcag actgatctct ctcaaggctg 300
agaaggatgg ggcagccact ggagtggatg ccatctgcac ccaccacctt aaccctcaaa 360
gccctggact ggacagggag cagctgtact ggcagctgag ccag
404

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<210> 534

<211> 157

<212> DNA

<213> Homo sapiens

<400> 534

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gacagagagc agctatactg ggagctgagc cagctaaccg acagcatcac tgagctgggc 120
ccctacaccg tggacagggg cagtctctat gtcaatg
157

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<210> 535

<211> 468

<212> DNA

<213> Homo sapiens

<400> 535

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tgctattcac tctcaacttc accatcacca acctgcggta tgaggagAAC atgcagcacc 180
ctggctccag gaagttcaac accacggaga gggctcttca gggcctgctc aggtccctgt 240
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gccctaggct ggacagagag cagctgtatt gggagctgag ccagctgacc cacaatatca 420
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468

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<210> 536

<211> 334

<212> DNA

<213> Homo sapiens

<400> 536

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tgggagcatc taagactcca gcctcgatat ttggcccttc agctgccagc catctcctga 120
tactattcac cctcaacttc accatcacta acctgcggta tgaggagAAC atgtggcctg 180
gtccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg ccctgtttca 240

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agaacaccag tgttggccct ctgtactctg gctgcaggct gaccttgctc aggccagaga 300
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<210> 537

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<212> DNA

<213> Homo sapiens

<400> 537

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<210> 538

<211> 468

<212> DNA

<213> Homo sapiens

<400> 538

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<211> 465

<212> DNA

<213> Homo sapiens

<400> 539

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<211> 255

<212> DNA

<213> Homo sapiens

<400> 540

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<210> 541

<211> 390

<212> DNA

<213> Homo sapiens

<400> 541

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<210> 542

<211> 468

<212> DNA

<213> Homo sapiens

<400> 542

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<210> 543

<211> 475

<212> DNA

<213> Homo sapiens

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<210> 544

<211> 485

<212> DNA

<213> Homo sapiens

<400> 544

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<210> 545

<211> 141
 <212> DNA
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<210> 546
 <211> 142
 <212> DNA
 <213> Homo sapiens

<400> 546
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 aaagacagcc tctaccttaa cg 142

<210> 547
 <211> 185
 <212> DNA
 <213> Homo sapiens

<400> 547
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 tctgacaaat ggcatccagg agctgggccc ctacaccctg gaccggaaca gtctctatgt 180
 caatg 185

<210> 548
 <211> 462
 <212> DNA
 <213> Homo sapiens

<400> 548
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<210> 549
 <211> 400
 <212> DNA
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<400> 549
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 ctcaacagag agcggctgta ctgggagctg agccaactga ccaatggcat caaagagctg 360
 ggcccctaca ccctggacag gaacagtctc tatgtcaatg 400

<210> 550
 <211> 468
 <212> DNA
 <213> Homo sapiens

<400> 550
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<210> 551
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 551
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 tcaatg 366

<210> 552
 <211> 465
 <212> DNA
 <213> Homo sapiens

<400> 552
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<210> 553
 <211> 401
 <212> DNA
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<400> 553
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 atactggggag ctgagccagc tgaccaatgg catcaaagaa a 401

<210> 554
 <211> 385
 <212> DNA
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<400> 554
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 gtacgaggag gacatgcac acccaggctc caggaagttc aacaccacgg agcgggtcct 180
 gcagggtctg cttgggtccca tgttcaagaa caccagtgtc ggccttctgt actctggctg 240
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<210> 555
 <211> 173
 <212> DNA
 <213> Homo sapiens

<400> 555
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 catcaaagag ctgggcccct acaccctgga ccggaacagt ctctacgtca atg 173

<210> 556
 <211> 468
 <212> DNA
 <213> Homo sapiens

<400> 556
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<210> 557
 <211> 468
 <212> DNA
 <213> Homo sapiens

<400> 557
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<210> 558
 <211> 468
 <212> DNA

<213> Homo sapiens

<400> 558

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<210> 559

<211> 468

<212> DNA

<213> Homo sapiens

<400> 559

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<210> 560

<211> 468

<212> DNA

<213> Homo sapiens

<400> 560

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<210> 561

<211> 468

<212> DNA

<213> Homo sapiens

<400> 561

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<210> 562

<211> 407

<212> DNA

<213> Homo sapiens

<400> 562

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gactggacag agagcgggtg tactggaagc tgagccagct gaccacggc atcactgagc 360
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<210> 563

<211> 468

<212> DNA

<213> Homo sapiens

<400> 563

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gccttgact ggacagagag cagctatact gggagctgag ccagctaacc cacagcatca 420
ctgagctggg ccctaacc ctggacaggg acagtctcta tgtcaatg 468
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<210> 564

<211> 468

<212> DNA

<213> Homo sapiens

<400> 564

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<210> 565

<211> 465

<212> DNA

<213> Homo sapiens

<400> 565

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<210> 566
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 566
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 gtctgcctat caagcaggtg ttccatgagc tgagccagca gacccatggc atcaccggc 360
 tgggccccta ctctctggac aaagacagcc tctaccttaa cg 402

<210> 567
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 567
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 acttcaccat ctccaatctc cagtattcac cagatatggg caagggctca gctacattca 180
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gagaaggatg gggcagccac yggagtggat gccatctgca cccaccgccy tgaccccaaa 360
agccctggac tggacagaga gcagctrta tgggagctga gccagctgac cmayrgcatc 420
amwgagctgg gccctacac cctggacagg racagtctct atgtcaatg 469

```

<210> 571

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 69, 107, 110

<223> Xaa = Any amino acid

<400> 571

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His Pro Gln Leu Glu Gln Gln Pro Gln Ser His Ser Trp Cys His Ser
          5                      10                      15

```

```

Pro Ser Thr Ser Thr His His Gln Pro Ala Val Arg Gly Gly His Ala
          20                      25                      30

```



```

<400> 573
Xaa Ser Pro Ala Arg Thr Ala Ala Thr Val Pro Phe Met Val Pro Phe
      5                      10                      15

Thr Leu Asn Phe Asn Ser Ser Pro Thr Cys Ser Thr Arg Arg Thr Cys
      20                      25                      30

Gly Thr Trp Phe Gln Glu Val Gln Arg Ala Gln Arg Glu Asn Cys Arg
      35                      40                      45

Val Val Leu Lys Pro Xaa Ile Arg Asn Ser Ser Leu Glu Tyr Leu Tyr
      50                      55                      60

Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala
      65                      70                      75                      80

Thr Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu
      85                      90                      95

Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn
      100                     105                     110

Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
      115                     120                     125

Val Asn
      130

```

<400> 574
Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr
 5 10 15

Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser
 20 25 30

Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg
 50 55 60
 Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu
 65 70 75 80
 Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95
 Leu Leu Arg Pro Xaa Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile
 100 105 110
 Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln
 115 120 125
 Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly
 130 135 140
 Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 145 150 155

<210> 575

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 103

<223> Xaa = Any amino acid

<400> 575

Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr
 5 10 15
 Ser Thr Val Asp Leu Arg Thr Ser Val Thr Pro Ser Ser Leu Ser Ser
 20 25 30
 Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
 35 40 45
 Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly
 50 55 60
 Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly
 65 70 75 80
 Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 85 90 95
 Leu Thr Ser Leu Arg Ser Xaa Lys Asp Gly Ala Ala Thr Gly Val Asp
 100 105 110

Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg
 115 120 125

Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu
 130 135 140

Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 145 150 155

<210> 576

<211> 122

<212> PRT

<213> Homo sapiens

<400> 576

Ala Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr
 5 10 15

Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
 20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Arg Gly Pro Met Phe Lys
 35 40 45

Asn Thr Ser Gly Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 50 55 60

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
 65 70 75 80

His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr
 85 90 95

Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
 100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 115 120

<210> 577

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 11,106,151

<223> Xaa = Any amino acid

<400> 577

Gly Phe Thr His Arg Thr Ser Val Pro Thr Xaa Ser Thr Pro Gly Thr
 5 10 15

Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser
 20 25 30

Pro	Ala	Thr	Ala	Gly	Pro	Leu	Leu	Val	Leu	Phe	Thr	Leu	Asn	Phe	Thr
		35					40					45			
Ile	Thr	Asn	Leu	Lys	Tyr	Glu	Glu	Asp	Met	His	Arg	Pro	Gly	Ser	Arg
	50					55					60				
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Thr	Leu	Leu	Gly	Pro	Met
65					70					75					80
Phe	Lys	Asn	Thr	Ser	Val	Gly	Leu	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr
				85					90					95	
Leu	Leu	Arg	Ser	Glu	Lys	Asp	Gly	Ala	Xaa	Thr	Gly	Val	Asp	Ala	Ile
			100					105					110		
Cys	Thr	His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Val	Asp	Arg	Glu	Gln
		115					120					125			
Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu	Gly
	130					135					140				
Pro	Tyr	Thr	Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn				
145					150					155					

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<210> 578
<211> 155
<212> PRT
<213> Homo sapiens
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<400> 578																
Gly	Phe	Thr	His	Trp	Ile	Pro	Val	Pro	Thr	Ser	Ser	Thr	Pro	Gly	Thr	
				5					10					15		
Ser	Thr	Val	Asp	Leu	Gly	Ser	Gly	Thr	Pro	Ser	Ser	Leu	Pro	Ser	Pro	
			20					25					30			
Thr	Thr	Ala	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	
		35					40					45				
Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	His	His	Pro	Gly	Ser	Arg	Lys	
	50					55					60					
Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Met	Phe	
65					70					75					80	
Lys	Asn	Thr	Ser	Val	Gly	Leu	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	
				85					90					95		
Leu	Arg	Pro	Glu	Lys	Asn	Gly	Ala	Ala	Thr	Gly	Met	Asp	Ala	Ile	Cys	
			100					105					110			
Ser	His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Gln	Leu	
		115					120					125				
Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Gly	Ile	Lys	Glu	Leu	Gly	Pro	
	130					135					140					

195

Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn
 145 150 155

<210> 579

<211> 155

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 52,138

<223> Xaa = Any amino acid

<400> 579

Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr
 5 10 15

Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
 20 25 30

Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
 35 40 45

Thr Asn Leu Xaa Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys
 50 55 60

Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly Pro Met Phe
 65 70 75 80

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 85 90 95

Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
 100 105 110

Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu
 115 120 125

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Xaa Ile Lys Glu Leu Gly Pro
 130 135 140

Tyr Thr Leu Asp Ser Asn Ser Leu Tyr Val Asn
 145 150 155

<210> 580

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 23

<223> Xaa = Any amino acid

<400> 580

Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr

				5					10					15	
Ser	Thr	Val	Asp	Leu	Gly	Xaa	Ser	Gly	Thr	Pro	Ser	Ser	Leu	Pro	Ser
				20					25					30	
Pro	Thr	Ser	Ala	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr
				35					40					45	
Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	His	His	Pro	Gly	Ser	Arg
				50					55					60	
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Met
				65					70					75	80
Phe	Lys	Asn	Thr	Ser	Val	Gly	Leu	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr
				85					90					95	
Leu	Leu	Arg	Pro	Glu	Lys	Asn	Gly	Ala	Ala	Thr	Gly	Met	Asp	Ala	Ile
				100					105					110	
Cys	Ser	His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Gln
				115					120					125	
Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Gly	Ile	Lys	Glu	Leu	Gly
				130					135					140	
Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn				
				145					150					155	

<400> 581

Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Ala	Pro	Thr	Ser	Thr	Pro	Gly	Thr	
				5					10					15		
Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Ser	Ser	Leu	Pro	Ser	
				20					25					30		
Pro	Thr	Thr	Ala	Val	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	
				35					40					45		
Ile	Thr	Asn	Leu	Gln	Tyr	Gly	Glu	Asp	Met	Arg	His	Pro	Gly	Ser	Arg	
				50					55					60		
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Leu	
				65					70					75		
Phe	Lys	Asn	Ser	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Ile	
				85					90					95		
Ser	Leu	Arg	Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	
				100					105					110		
Cys	Thr	His	His	Leu	Asn	Pro	Gln	Ser	Pro	Gly	Leu	Asp	Arg	Glu	Gln	

197

115	120	125
Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly		
130	135	140
Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn		
145	150	155

<210> 582
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> 151
 <223> Xaa = Any amino acid

<400> 582
Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr
5 10 15
Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser
20 25 30
Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
35 40 45
Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg
50 55 60
Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile
65 70 75 80
Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95
Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val
100 105 110
Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln
115 120 125
Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
130 135 140
Pro Tyr Ser Leu Asp Arg Xaa Ser Leu Tyr Val Asn
145 150 155

<210> 583
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant

<222> 109,114,117,128,139

<223> Xaa = Any amino acid

<400> 583

Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
5 10 15

Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly
20 25 30

His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr
35 40 45

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu
65 70 75 80.

Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95

Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Xaa Asp Thr Ile
100 105 110

Cys Xaa His Arg Xaa Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Xaa
115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Xaa Ile Thr Glu Leu Gly
130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
145 150 155

<210> 584

<211> 156

<212> PRT

<213> Homo sapiens

<400> 584

Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
5 10 15

Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly
20 25 30

His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr
35 40 45

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu
65 70 75 80

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95

Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile
 100 105 110

Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly
 130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155

<210> 585

<211> 156

<212> PRT

<213> Homo sapiens

<400> 585

Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr
 5 10 15

Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly
 20 25 30

His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg
 50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu
 65 70 75 80

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95

Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile
 100 105 110

Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln
 115 120 125

Leu Tyr Trp Glu Leu Ser Lys Leu Thr Cys Gly Ile Ile Glu Leu Gly
 130 135 140

Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn
 145 150 155

<210> 586

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

200

<222> 151,156

<223> Xaa = Any amino acid

<400> 586

Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr Pro Gly Thr
 5 10 15

 Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg
 20 25 30

 Pro Ile Val Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45

 Ile Thr Asn Leu Gln Tyr Glu Glu Ala Met Arg His Pro Gly Ser Arg
 50 55 60

 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu
 65 70 75 80

 Phe Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr
 85 90 95

 Leu Leu Arg Pro Glu Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile
 100 105 110

 Cys Thr His His Pro Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln
 115 120 125

 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly
 130 135 140

 Pro Tyr Thr Leu Asp Arg Xaa Ser Leu Tyr Val Xaa
 145 150 155

<210> 587

<211> 156

<212> PRT

<213> Homo sapiens

<400> 587

Gly Phe Thr His Trp Ser Pro Ile Pro Thr Thr Ser Thr Pro Gly Thr
 5 10 15

 Ser Ile Val Asn Leu Gly Thr Ser Gly Ile Pro Pro Ser Leu Pro Glu
 20 25 30

 Thr Thr Ala Thr Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45

 Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly Ser Arg
 50 55 60

 Lys Phe Asn Ile Thr Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu
 65 70 75 80

 Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95

201

Leu Leu Arg Pro Glu Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile
 100 105 110

Cys Thr His Arg Pro Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly
 130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155

<210> 588

<211> 156

<212> PRT

<213> Homo sapiens

<400> 588

Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
 5 10 15

Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro Ser Ser Leu Pro Gly
 20 25 30

Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn Phe Thr
 35 40 45

Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg
 50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu
 65 70 75 80

Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95

Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val
 100 105 110

Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg
 115 120 125

Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly
 130 135 140

Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn
 145 150 155

<210> 589

<211> 156

<212> PRT

<213> Homo sapiens

<400> 589

Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr

202

				5						10					15				
Ser	Thr	Met	His	Leu	Ala	Thr	Ser	Arg	Thr	Pro	Ala	Ser	Leu	Ser	Gly				
			20					25					30						
Pro	Thr	Thr	Ala	Ser	Pro	Leu	Leu	Val	Leu	Phe	Thr	Ile	Asn	Phe	Thr				
		35					40					45							
Ile	Thr	Asn	Leu	Arg	Tyr	Glu	Glu	Asn	Met	His	His	Pro	Gly	Ser	Arg				
	50					55					60								
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Val				
65					70					75					80				
Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr				
				85					90					95					
Leu	Leu	Arg	Pro	Lys	Lys	Asp	Gly	Ala	Ala	Thr	Lys	Val	Asp	Ala	Ile				
			100					105						110					
Cys	Thr	Tyr	Arg	Pro	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asp	Arg	Glu	Gln				
	115						120					125							
Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly				
	130					135					140								
Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn								
145					150					155									

<210> 590

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 145

<223> Xaa = Any amino acid

<400> 590

Gly	Phe	Thr	Gln	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr				
				5					10					15					
Pro	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Val	Ser	Lys	Pro	Gly				
		20						25					30						
Pro	Ser	Ala	Ala	Ser	Pro	Leu	Leu	Val	Leu	Phe	Thr	Leu	Asn	Phe	Thr				
		35					40					45							
Ile	Thr	Asn	Leu	Arg	Tyr	Glu	Glu	Asn	Met	Gln	His	Pro	Gly	Ser	Arg				
	50					55					60								
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Ser	Leu				
65					70					75					80				
Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr				
				85					90					95					

Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile
 100 105 110

Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
 130 135 140

Xaa Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn
 145 150 155

<210> 591

<211> 155

<212> PRT

<213> Homo sapiens

<400> 591

Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr
 5 10 15

Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly
 20 25 30

Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr
 35 40 45

Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys
 50 55 60

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe
 65 70 75 80

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 85 90 95

Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys
 100 105 110

Thr His Arg Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu
 115 120 125

Tyr Leu Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
 130 135 140

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155

<210> 592

<211> 134

<212> PRT

<213> Homo sapiens

<400> 592

Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly Val Val

204

5							10							15		
Ser	Glu	Glu	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Asn	Asn	Leu	Arg	Tyr	
			20				25						30			
Met	Ala	Asp	Met	Gly	Gln	Pro	Gly	Ser	Leu	Lys	Phe	Asn	Ile	Thr	Asp	
			35				40				45					
Asn	Val	Met	Lys	His	Leu	Leu	Ser	Pro	Leu	Phe	Gln	Arg	Ser	Ser	Leu	
			50				55				60					
Gly	Ala	Arg	Tyr	Thr	Gly	Cys	Arg	Val	Ile	Ala	Leu	Arg	Ser	Val	Lys	
65				70						75			80			
Asn	Gly	Ala	Glu	Thr	Arg	Val	Asp	Leu	Leu	Cys	Thr	Tyr	Leu	Gln	Pro	
			85						90			95				
Leu	Ser	Gly	Pro	Gly	Leu	Pro	Ile	Lys	Gln	Val	Phe	His	Glu	Leu	Ser	
			100				105						110			
Gln	Gln	Thr	His	Gly	Ile	Thr	Arg	Leu	Gly	Pro	Tyr	Ser	Leu	Asp	Lys	
			115				120						125			
Asp	Ser	Leu	Tyr	Leu	Asn											
			130													

<210> 593

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 7

<223> Xaa = Any amino acid

<400> 593

Gly	Tyr	Asn	Glu	Pro	Gly	Xaa	Asp	Glu	Pro	Pro	Thr	Thr	Pro	Lys	Pro	
				5					10					15		
Ala	Thr	Thr	Phe	Leu	Pro	Pro	Leu	Ser	Glu	Ala	Thr	Thr	Ala	Met	Gly	
				20					25					30		
Tyr	His	Leu	Lys	Thr	Leu	Thr	Leu	Asn	Phe	Thr	Ile	Ser	Asn	Leu	Gln	
			35				40				45					
Tyr	Ser	Pro	Asp	Met	Gly	Lys	Gly	Ser	Ala	Thr	Phe	Asn	Ser	Thr	Glu	
			50				55				60					
Gly	Val	Leu	Gln	His	Leu	Leu	Arg	Pro	Leu	Phe	Gln	Lys	Ser	Ser	Met	
		65			70					75					80	
Gly	Pro	Phe	Tyr	Leu	Gly	Cys	Gln	Leu	Ile	Ser	Leu	Arg	Pro	Glu	Lys	
				85					90					95		
Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Thr	Thr	Cys	Thr	Tyr	His	Pro	Asp	
			100							105				110		

Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser
 115 120 125

Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg
 130 135 140

Asp Ser Leu Phe Ile Asn
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<210> 594

<211> 318

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 136,248,268

<223> Xaa = Any amino acid

<400> 594

Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn
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Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser
 20 25 30

Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu
 35 40 45

Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr
 50 55 60

Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser
 65 70 75 80

Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr
 85 90 95

Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp
 100 105 110

Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser
 115 120 125

Ser Ser Thr Gln His Phe Tyr Xaa Asn Phe Thr Ile Thr Asn Leu Pro
 130 135 140

Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn
 145 150 155 160

Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser
 165 170 175

Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val
 180 185 190

206

Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro
 195 200 205

Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg
 210 215 220

Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser
 225 230 235 240

Ser Val Leu Val Asp Gly Tyr Xaa Pro Asn Arg Asn Glu Pro Leu Thr
 245 250 255

Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Xaa Ile Gly Leu Ala
 260 265 270

Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr
 275 280 285

Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys
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Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
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<210> 595

<211> 3451

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560, 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401

<223> Xaa = Any Amino Acid

<400> 595

Ile Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala
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Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Thr Ala Val Asp Ala Ile
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Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg
 35 40 45

Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly
 50 55 60

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His
 65 70 75 80

Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp
 85 90 95

Val Gly Thr Ser Gly Thr Pro Ser Ser Pro Ser Pro Thr Thr Ala
 100 105 110

Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
 115 120 125

Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr
 130 135 140

Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr
 145 150 155 160

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro

				165					170					175			
Xaa	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg		
			180					185					190				
Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Gln	Leu	Tyr	Trp	Glu		
		195					200					205					
Leu	Ser	Lys	Leu	Thr	Asn	Asp	Ile	Glu	Glu	Leu	Gly	Pro	Tyr	Thr	Leu		
		210				215					220						
Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Gln	Ser	Ser	Val		
225					230					235					240		
Ser	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	Asp	Leu	Arg	Thr	Ser		
				245						250				255			
Val	Thr	Pro	Ser	Ser	Leu	Ser	Ser	Pro	Thr	Ile	Met	Ala	Ala	Gly	Pro		
			260					265					270				
Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr		
		275					280					285					
Gly	Glu	Asp	Met	Gly	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu		
		290				295					300						
Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Ile	Phe	Lys	Asn	Thr	Ser	Val		
305				310						315					320		
Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Ser	Leu	Arg	Ser	Xaa	Lys		
				325					330					335			
Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Ile	His	His	Leu	Asp		
			340					345					350				
Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Arg	Leu	Tyr	Trp	Glu	Leu	Ser		
		355					360					365					
Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg		
		370				375					380						
Asn	Ser	Leu	Tyr	Val	Asn	Ala	Ala	Gly	Pro	Leu	Val	Leu	Phe	Thr			
385				390					395					400			
Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Lys	Tyr	Glu	Glu	Asp	Met	His	Arg		
				405					410					415			
Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Thr	Leu		
			420					425					430				
Arg	Gly	Pro	Met	Phe	Lys	Asn	Thr	Ser	Gly	Gly	Leu	Leu	Tyr	Ser	Gly		
		435					440					445					
Cys	Arg	Leu	Thr	Leu	Leu	Arg	Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly		
		450				455					460						
Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Val		
465				470					475					480			
Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Gly	Ile		
				485					490					495			
Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn		
			500					505					510				
Gly	Phe	Thr	His	Arg	Thr	Ser	Val	Pro	Thr	Xaa	Ser	Thr	Pro	Gly	Thr		
		515					520										

625					630					635				640
Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu
				645					650					655
Pro	Tyr	Thr	Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr
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Trp	Ile	Pro	Val	Pro	Thr	Ser	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val
			675				680					685		
Leu	Gly	Ser	Gly	Thr	Pro	Ser	Ser	Leu	Pro	Ser	Pro	Thr	Thr	Ala
			690			695					700			
Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu
705					710					715				720
Tyr	Glu	Glu	Asp	Met	His	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr
			725					730					735	
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Met	Phe	Lys	Asn	Thr
			740					745				750		
Val	Gly	Leu	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro
		755				760					765			
Lys	Asn	Gly	Ala	Ala	Thr	Gly	Met	Asp	Ala	Ile	Cys	Ser	His	Arg
	770					775					780			
Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Gln	Leu	Tyr	Trp	Glu
785					790				795					800
Ser	Gln	Leu	Thr	His	Gly	Ile	Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu
			805					810					815	
Arg	His	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Trp	Ile	Pro	Val
			820					825					830	
Thr	Ser	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	Asp	Leu	Gly	Ser	Gly
		835				840						845		
Pro	Ser	Ser	Leu	Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu	Leu	Val
		850			855					860				
Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Xaa	Tyr	Glu	Glu	Asp
865					870				875					880
His	Cys	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu
			885					890					895	
Ser	Leu	Leu	Gly	Pro	Met	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu
			900				905					910		
Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Ser	Glu	Lys	Asp	Gly	Ala
		915				920					925			
Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Leu	Asp	Pro	Lys	Ser
		930				935					940			
Gly	Val	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr
945					950				955					960
Xaa	Ile	Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Ser	Asn	Ser	Leu
			965					970					975	
Val	Asn	Gly	Phe	Thr	His	Gln	Thr	Ser	Ala	Pro	Asn	Thr	Ser	Thr
			980				985					990		
Gly	Thr	Ser	Thr	Val	Asp	Leu	Gly	Xaa	Ser	Gly	Thr	Pro	Ser	Ser
		995				1000					1005			
Pro	Ser	Pro	Thr	Ser	Ala	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu
		1010				1015				1020				
Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	His	His	Pro
1025					1030				1035					1040
Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu
			1045					1050					1055	
Pro	Met	Phe	Lys	Asn	Thr	Ser	Val	Gly	Leu	Leu	Tyr	Ser	Gly	Cys
		1060				1065					1070			
Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asn	Gly	Ala	Ala	Thr	Gly	Met
		1075				1080					1085			
Ala	Ile	Cys	Ser	His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asn

1090	1095	1100
Glu Gln Leu Tyr Trp	Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu	
1105	1110	1115
Leu Gly Pro Tyr Thr	Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe	1120
	1125	1130
Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr		1135
	1140	1145
Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr		1150
	1155	1160
Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr		1165
	1170	1175
Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe		1180
1185	1190	1195
Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys		1200
	1205	1210
Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu		1215
	1220	1225
Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr		1230
	1235	1240
His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr		1245
	1250	1255
Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr		1260
1265	1270	1275
Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser		1280
	1285	1290
Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly		1295
	1300	1305
Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro		1310
	1315	1320
Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr		1325
	1330	1335
Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu		1340
1345	1350	1355
Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val		1360
	1365	1370
Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys		1375
	1380	1385
Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn		1390
	1395	1400
Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser		1405
	1410	1415
Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg		1420
1425	1430	1435
Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr		1440
	1445	1450
Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr		1455
	1460	1465
Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro		1470
	1475	1480
Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met		1485
	1490	1495
Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln		1500
1505	1510	1515
Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr		1520
	1525	1530
Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala		1535
	1540	1545
Thr Gly Xaa Asp Thr Ile Cys Xaa His Arg Xaa Asp Pro Ile Gly Pro		1550

1555	1560	1565
Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Gln Leu Thr His		
1570	1575	1580
Xaa Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr		
1585	1590	1595
Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro		
1605	1610	1615
Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu		
1620	1625	1630
Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn		
1635	1640	1645
Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly		
1650	1655	1660
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys		
1665	1670	1675
Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg		
1685	1690	1695
Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp		
1700	1705	1710
Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg		
1715	1720	1725
Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu		
1730	1735	1740
Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe		
1745	1750	1755
Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala		
1765	1770	1775
Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr		
1780	1785	1790
Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr		
1795	1800	1805
Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe		
1810	1815	1820
Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys		
1825	1830	1835
Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu		
1845	1850	1855
Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr		
1860	1865	1870
His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr		
1875	1880	1885
Trp Glu Leu Ser Lys Leu Thr Cys Gly Ile Ile Glu Leu Gly Pro Tyr		
1890	1895	1900
Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn		
1905	1910	1915
Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly		
1925	1930	1935
Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro		
1940	1945	1950
Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr		
1955	1960	1965
Glu Glu Ala Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu		
1970	1975	1980
Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Ile		
1985	1990	1995
Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys		
2005	2010	2015
Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro Asp		

2020										2025					2030				
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2035							2040					2045							
Gln	Leu	Thr	His	Gly	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg				
2050						2055					2060								
Xaa	Ser	Leu	Tyr	Val	Xaa	Gly	Phe	Thr	His	Trp	Ser	Pro	Ile	Pro	Thr				
2065					2070					2075					2080				
Thr	Ser	Thr	Pro	Gly	Thr	Ser	Ile	Val	Asn	Leu	Gly	Thr	Ser	Gly	Ile				
				2085					2090					2095					
Pro	Pro	Ser	Leu	Pro	Glu	Thr	Thr	Ala	Thr	Gly	Pro	Leu	Leu	Val	Pro				
2100							2105					2110							
Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asn	Met				
2115						2120					2125								
Gly	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Ile	Thr	Glu	Ser	Val	Leu	Gln				
2130						2135				2140									
Gly	Leu	Leu	Lys	Pro	Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr				
2145				2150				2155							2160				
Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Val	Ala				
2165							2170							2175					
Thr	Arg	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Pro	Asp	Pro	Lys	Ile	Pro				
2180							2185						2190						
Gly	Leu	Asp	Arg	Gln	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His				
2195						2200					2205								
Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr				
2210						2215				2220									
Val	Asn	Gly	Phe	Thr	Gln	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr	Pro				
2225				2230				2235							2240				
Gly	Thr	Phe	Thr	Val	Gln	Pro	Glu	Thr	Ser	Glu	Thr	Pro	Ser	Ser	Leu				
2245							2250							2255					
Pro	Gly	Pro	Thr	Ala	Thr	Gly	Pro	Val	Leu	Leu	Pro	Phe	Thr	Leu	Asn				
2260							2265					2270							
Phe	Thr	Ile	Ile	Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	His	Arg	Pro	Gly				
2275						2280					2285								
Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Met				
2290						2295					2300								
Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Ser	Ser	Leu	Tyr	Ser	Gly	Cys	Arg				
2305				2310				2315							2320				
Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Arg	Val	Asp				
2325							2330							2335					
Ala	Val	Cys	Thr	His	Arg	Pro	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asp	Arg				
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Glu	Arg	Leu	Tyr	Trp	Lys	Leu	Ser	Gln	Leu	Thr	His	Gly	Ile	Thr	Glu				
2355						2360					2365								
Leu	Gly	Pro	Tyr																

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Tyr	Arg	Pro	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr		
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Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr		
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Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	Gln	Arg	Ser		
	2530				2535					2540							
Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr	Pro	Thr	Val	Asp	Leu	Gly		
2545				2550				2555							2560		
Thr	Ser	Gly	Thr	Pro	Val	Ser	Lys	Pro	Gly	Pro	Ser	Ala	Ala	Ser	Pro		
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Leu	Leu	Val	Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Arg	Tyr		
		2580					2585					2590					
Glu	Glu	Asn	Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu		
	2595					2600					2605						
Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Ser	Leu	Phe	Lys	Ser	Thr	Ser	Val		
	2610				2615					2620							
Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys		
2625				2630					2635						2640		
Asp	Gly	Thr	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	His	Pro	Asp		
			2645					2650						2655			
Pro	Lys	Ser	Pro	Arg	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu	Ser		
		2660						2665					2670				
Gln	Leu	Thr	His	Asn	Ile	Thr	Glu	Leu	Gly	Xaa	Tyr	Ala	Leu	Asp	Asn		
	2675					2680					2685						
Asp	Ser	Leu	Phe	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Ser	Thr		
	2690				2695						2700						
Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Val	Tyr	Leu	Gly	Ala	Ser	Lys	Thr		
2705				2710						2715					2720		
Pro	Ala	Ser	Ile	Phe	Gly	Pro	Ser	Ala	Ala	Ser	His	Leu	Leu	Ile	Leu		
			2725					2730						2735			
Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Arg	Tyr	Glu	Glu	Asn	Met		
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Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly		
	2755					2760					2765						
Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser		
	2770				2775						2780						
Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Glu	Ala	Thr		
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Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Pro	Asp	Pro	Thr	Gly	Pro	Gly		
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<212> PRT

<213> Homo sapiens

<400> 596

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 Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser
 20 25 30

 Pro Thr Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45

 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg
 50 55 60

 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu
 65 70 75 80

 Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95

 Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile
 100 105 110

 Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln
 115 120 125

 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly
 130 135 140

 Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155

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International Bureau(43) International Publication Date
24 January 2002 (24.01.2002)

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C12N 15/12, 15/85, 5/10, C07K 16/30, G01N 33/574,
C12Q 1/68, C12N 15/62, 5/06, A61K 39/00, 39/395(71) Applicant (for all designated States except US): CORIXA
CORPORATION [US/US]; 1124 Columbia Street, Suite
200, Seattle, WA 98104 (US).

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(72) Inventors; and

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(75) Inventors/Applicants (for US only): MITCHAM, Jen-
nifer, L. [US/US]; 16677 N.E. 88th Street, Redmond, WA
98052 (US). KING, Gordon, E. [US/US]; 15716 First
Avenue N.W., Shoreline, WA 98177 (US). ALGATE,
Paul, A. [GB/US]; 580 Kalmia Place N.W., Issaquah,
WA 98027 (US). FLING, Steven, P. [US/US]; 11414
Pinyon Avenue N.E., Bainbridge Island, WA 98110 (US).
RETTTER, Marc, W. [US/US]; 33402 N.E. 43rd Place,
Carnation, WA 98014 (US). FANGER, Gary, Richard
[US/US]; 15906 29th Drive S.E., Mill Creek, WA 98012
(US). REED, Steven, G. [US/US]; 2843 122nd Place
N.E., Bellevue, WA 98005 (US). VEDVICK, Thomas,
S. [US/US]; 124 S. 300th Place, Federal Way, WA 98003
(US). CARTER, Darrick [US/US]; 321 Summit Avenue
E., Seattle, WA 98102 (US). HILL, Paul [US/US]; 4917

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[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

11729.1 contg

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11729-45.21.21.cons1

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11729-45.21.21.cons2

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11731.1contg

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CTTCTGTTGCTCT

(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as ovarian cancer, are disclosed. Compositions may comprise one or more ovarian carcinoma proteins, immunogenic portions thereof, polynucleotides that encode such portions or antibodies or immune system cells specific for such proteins. Such compositions may be used, for example, for the prevention and treatment of diseases such as ovarian cancer. Methods are further provided for identifying tumor antigens that are secreted from ovarian carcinomas and/or other tumors. Polypeptides and polynucleotides as provided herein may further be used for the diagnosis and monitoring of ovarian cancer.

WO 02/006317 A3



West View Drive, Everett, WA 98201 (US). ALBONE, Earl [US/US]; 509 Launfall Road, Plymouth Meeting, PA 19462 (US).

(74) Agents: POTTER, Jane, E., R.; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 et al. (US).

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Published:

— with international search report

(88) Date of publication of the international search report:

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/22635

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C07K14/47 C12N15/12 C12N15/85 C12N5/10 C07K16/30
 G01N33/574 C12Q1/68 C12N15/62 C12N5/06 A61K39/00
 A61K39/395

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N G01N C12Q A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

EP0-Internal, WPI Data, PAJ, BIOSIS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00 36107 A (CORIXA CORP) 22 June 2000 (2000-06-22) SEQ ID NO:311, 312, 385-390 encoding 0772P polynucleotides and polypeptides pages 48, 50, 51 claims 1,2,7,8,13-17,21,33,37,39,42,49 -----	1-3,7, 15, 19-32,35
A	SCHUMMER MICHEL ET AL: "Comparative hybridization of an array of 21 500 ovarian cDNAs for the discovery of genes overexpressed in ovarian carcinomas." GENE (AMSTERDAM), vol. 238, no. 2, 1 October 1999 (1999-10-01), pages 375-385, XP002222131 ISSN: 0378-1119 the whole document -----	1,7,24, 25,32

☐ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"a" document member of the same patent family

Date of the actual completion of the international search

11 December 2002

Date of mailing of the international search report

01 04 2003

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
 NL - 2280 HV Rijswijk
 Tel. (+31-70) 340-2040, Tx. 31.651 epo nl,
 Fax: (+31-70) 340-3016

Authorized officer

Brouns, G

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US 01/22635

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3, 7, 15, 19-32, 35 all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claims 25 and 32 are directed to a diagnostic method practised on the human or animal body, the search has been carried out and based on the alleged effects of the composition.

Although claims 27, 30 and 31 are directed to a method of treatment of the human or animal body, the search has been carried out and based on the alleged effects of the composition.

Continuation of Box I.2

Present claims 1-11 and 15-19 relate to an extremely large number of possible compounds. In fact, the claims contain so many options for an ovarian carcinoma antigen 0772P that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search has been carried out for those parts of the application which do appear to be clear and concise.

In view of the description (page 5, line 28-page 6, line 5), an 0772P consensus repeat sequence 'X' as set forth in SEQ ID NO:596 is considered to be a sequence element of 156 amino acids. As a consequence, the search has been limited to an 0772P polypeptide comprising an X repeat 'consisting' of a sequence as defined by the claimed SEQ ID NOs in the application.

Present claim 25 relates to an agent defined by reference to a desirable characteristic or property, namely that it binds to a polypeptide of claim 21.

The claim covers all agents having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and disclosure within the meaning of Article 5 PCT for only a very limited number of such agents. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the agents by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely those parts relating to antibodies binding to a polypeptide of claim 21.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-3,7,15,19-32,35, all partially

Invention 1

An 0772P polypeptide having the structure X-Y, wherein X comprises the sequence defined by SEQ ID NO:574 and Y comprises a sequence having at least 80% identity with the sequence of SEQ ID NO:594, a polynucleotide encoding said X repeat defined by SEQ ID NO:542, said polypeptide or polynucleotide being overexpressed in ovarian cancer cells compared with normal tissue, an isolated nucleic acid sequence defined by SEQ ID NO:542, complement thereof, sequence containing at least 20 contiguous residues thereof, sequences that hybridise to said sequence, sequence having at least 75% or 90% identity to said sequence, degenerate variants of said sequence, polypeptides encoded by said sequence, said sequence in an expression vector, a host cell transfected with said expression vector, an isolated antibody binding aforementioned polypeptide, a method of diagnosing cancer using said peptide, a fusion protein comprising said peptide, a method for stimulating or expanding T cells using said polynucleotides or polypeptides and the resulting T cell population, a composition comprising said polynucleotide, polypeptide, antibody, fusion protein, T cell population or antigen presenting cells expressing the polypeptide, a method for stimulating an immune response, a method for treatment of ovarian cancer, a method of determining ovarian cancer in a patient and an antibody against the specific 0772P polypeptide of the invention.

2. Claims: 1-3,7,35, all partially

Inventions 2-20

As for invention 1, but limited to subject-matter relating to polypeptides having an X domain as defined in SEQ ID NOs 575-593, whereby invention 2 is limited to SEQ ID NO:575, invention 3 is limited to SEQ ID NO:576, invention 4 is limited to SEQ ID NO:577, etc..., invention 19 is limited to SEQ ID NO:592 and invention 20 is limited to SEQ ID NO:593

3. Claims: 15 and 19-32, all partially

Invention 21

A polynucleotide encoding an 0772P polypeptide having the structure X-Y, whereby X and Y are encoded by the sequence defined by SEQ ID NO:512 and SEQ ID NO:568, respectively, said polypeptide overexpressed in ovarian cancer cells

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

compared with normal tissue and an isolated nucleic acid sequence defined by SEQ ID NO:512, complement thereof, sequence containing at least 20 contiguous residues thereof, sequences that hybridise to said sequence, sequence having at least 75% or 90% identity to said sequence, degenerate variants of said sequence, polypeptides encoded by said sequence, said sequence in an expression vector, a host cell transfected with said expression vector, an isolated antibody binding aforementioned polypeptide, a method of diagnosing cancer using said peptide, a fusion protein comprising said peptide, a method for stimulating or expanding T cells using said polynucleotides or polypeptides and the resulting T cell population, a composition comprising said polynucleotide, polypeptide, antibody, fusion protein, T cell population or antigen presenting cells expressing the polypeptide, a method for stimulating an immune response, a method for treatment of ovarian cancer and a method of determining ovarian cancer in a patient.

4. Claims: 15 and 19-32, all partially

Inventions 22-73

As for invention 21, but limited to the subject-matter relating to an X domain encoding polynucleotide as defined in SEQ ID NOs:513-540, 543-546 and 548-567, whereby invention 22 is limited to SEQ ID NO:513, invention 23 is limited to SEQ ID NO:514, invention 24 is limited to SEQ ID NO:515,, invention 49 is limited to SEQ ID NO:540, invention 50 is limited to SEQ ID NO:543, invention 51 is limited to SEQ ID NO:544, invention 52 is limited to SEQ ID NO:545, invention 53 is limited to SEQ ID NO:546, invention 54 is limited to SEQ ID NO:548, invention 55 is limited to SEQ ID NO:549, ..., invention 72 is limited to SEQ ID NO:566 and invention 73 is limited to SEQ ID NO:567

5. Claims: 20-32, all partially

Invention 74

Isolated nucleic acid sequence defined by SEQ ID NO:464, complement thereof, sequence containing at least 20 contiguous residues thereof, sequences that hybridise to said sequence, sequence having at least 75% or 90% identity to said sequence, degenerate variants of said sequence, polypeptides encoded by said sequence, said sequence in an expression vector, a host cell transfected with said expression vector, an isolated antibody binding aforementioned polypeptide, a method of diagnosing cancer using said peptide, a fusion protein comprising said peptide, a method for stimulating or expanding T cells using said polynucleotides or polypeptides and the resulting T cell population, a composition comprising said

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

polynucleotide, polypeptide, antibody, fusion protein, T cell population or antigen presenting cells expressing the polypeptide, a method for stimulating an immune response, a method for treatment of ovarian cancer and a method of determining ovarian cancer in a patient.

6. Claims: 20-32, all partially

Inventions 75-91

As for invention 74, but limited to the subject-matter relating to an nucleic acid sequence as defined in SEQ ID NOs:465-477, 541, 547, 568 and 569, wherein invention 75 is limited to SEQ ID NO:465, invention 76 is limited to SEQ ID NO:466, invention 77 is limited to SEQ ID NO:467, invention 78 is limited to SEQ ID NO:468, invention 79 is limited to SEQ ID NO:469, invention 80 is limited to SEQ ID NO:470, invention 81 is limited to SEQ ID NO:471, invention 82 is limited to SEQ ID NO:472, invention 83 is limited to SEQ ID NO:473, invention 84 is limited to SEQ ID NO:474, invention 85 is limited to SEQ ID NO:475, invention 86 is limited to SEQ ID NO:476, invention 87 is limited to SEQ ID NO:477, invention 88 is limited to SEQ ID NO:541, invention 89 is limited to SEQ ID NO:547, invention 90 is limited to SEQ ID NO:568, invention 91 is limited to SEQ ID NO:569

7. Claims: 33, partially

Invention 92

An 0772P polypeptide comprising at least an antibody epitope sequence set forth in SEQ ID NO:490

8. Claims: 33, partially

Inventions 93-113

As for invention 92, but limited to the subject-matter relating to an antibody epitope as defined in SEQ ID NOs:491-511, wherein invention 93 is limited to SEQ ID NO:491, invention 94 is limited to SEQ ID NO:492,, invention 113 is limited to SEQ ID NO:511

9. Claims: 34, partially

Invention 114

An 08E polypeptide comprising at least an antibody epitope sequence set forth in SEQ ID NO:394

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

10. Claims: 34, partially

Inventions 115-135

As for invention 114, but limited to the subject-matter relating to an antibody epitope as defined in SEQ ID NOs:395-415, wherein invention 115 is limited to SEQ ID NO:395, invention 116 is limited to SEQ ID NO:396,, invention 135 is limited to SEQ ID NO:415

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/22635

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0036107	A	22-06-2000	
		US 6528253 B1	04-03-2003
		US 6488931 B1	03-12-2002
		US 6468546 B1	22-10-2002
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		TR 200102507 T2	21-01-2002
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		US 2002119158 A1	29-08-2002

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